



STIC Search Report

Biotech-Chem Library

STIC Database Tracking Number: 157955

TO: Jegatheesan Seharaseyon
Art Unit: 1647
Location: REM-4C61/4C70
Serial Number: 09/658677

Thursday, July 07, 2005

From: Beverly Shears
Location: Biotech-Chem Library
REM 1A54
Phone: 571-272-2528
beverly.shears@uspto.gov

Search Notes

Protein Sequence Searches – February 2005

All of the sequence databases on ABSS have recently been updated.

- Please note that the curators of the UniProt database have purged some temporary accession numbers from the most recent version of UniProt. These sequences have been assigned new permanent accession numbers. The new UniProt record may not contain the previous temporary accession number.
- If you encounter an accession number from an older search run against UniProt (results file extension **.rup**) that can no longer be found in the database, the permanent record with the new accession number can be found by searching the old accession number in the UniProt Protein Archive database (uniPARC) at:

<http://www.pir.uniprot.org/database/archive.shtml>

If you have any questions regarding this information or your results, please contact any STIC searcher.



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157955

LB

From: Seharaseyon, Jegatheesan
Sent: Thursday, June 30, 2005 9:27 AM
To: STIC-Biotech/ChemLib
Subject: RE:09/658677

CRFE

Hi,

Please search SEQ ID NO: 2, 15 and 18 of 09/658,677
in the interference and commercial databases.

Thanks.
Seyon.

J. Seharaseyon
Art Unit 1647
Remsen 4C61
Mailbox 4C70
Phone: (571)-272-0892
Fax: (571)-273-0892

2 - 392 AA
15 - 392
18 - 383 AF

STAFF USE ONLY

Searcher: _____
Searcher Phone: 2-_____
Date Searcher Picked up: _____
Date Completed: _____
Searcher Prep/Rev. Time: _____
Online Time: _____

Type of Search

NA#: _____ AA#: _____
Interference: _____ SPDI: _____
S/L: _____ Oligomer: _____
Encode/Transl: _____
Structure#: _____ Text: _____
Inventor: _____ Litigation: _____

Vendors and cost where applicable

STN: _____
DIALOG: _____
QUESTEL/ORBIT: _____
LEXIS/NEXIS: _____
SEQUENCE SYSTEM: _____
WWW/Internet: _____
Other(Specify): _____

Date completed: _____

Searcher: Beverly e 2528

Terminal time: _____

Elapsed time: _____

CPU time: _____

Total time: _____

Number of Searches: _____

Number of Databases: _____

Search Site

_____ STIC

_____ CM-1

_____ Pre-S

Type of Search

_____ N.A. Sequence

_____ A.A. Sequence

_____ Structure

_____ Bibliographic

Vendors

_____ IG

_____ STN

_____ Dialog

_____ APS

_____ Geninfo

_____ SDC

_____ DARC/Questel

_____ Other CGN

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: July 1, 2005, 20:52:53 ; Search time 100.435 Seconds
(without alignments)
1509.530 Million cell updates/sec

Title: US-09-658-677-2

Perfect score: 2112

Sequence: 1 MAGIPGLFLFLFLCAVGO.....IKGNVLDREGDVFVLPQSN 392

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_16Dec04:*
1: Geneseq1980s:*
2: Geneseq1990s:*
3: Geneseq2000s:*
4: Geneseq2001s:*
5: Geneseq2002s:*
6: Geneseq2003as:*
7: Geneseq2003bs:*
8: Geneseq2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2104	99.6	392	4	AAB48972 Human Zsi
2	2085	98.7	392	4	AAB48973 Human Zsi
3	2044	96.8	383	2	AAY08660 WO9927094
4	2044	96.8	383	2	AAY08657 Human tra
5	2044	96.8	383	2	AAY13390 Amino aci
6	2044	96.8	383	3	AAY88277 Human TAN
7	2044	96.8	383	3	AAY87270 Human sig
8	2044	96.8	383	3	AAY53627 A bone ma
9	2044	96.8	383	3	AAB25618 Protein e
10	2044	96.8	383	3	AAB25592 Protein e
11	2044	96.8	383	3	ADC78573 Human PRO
12	2044	96.8	383	4	AAB80258 Human PRO
13	2044	96.8	383	4	AAB48974 Human Zsi
14	2044	96.8	383	4	AAB29048 Human PRO
15	2044	96.8	383	6	ABU58424 Human PRO
16	2044	96.8	383	6	ABU71636 Human PRO
17	2044	96.8	383	6	ABU87972 Novel hum
18	2044	96.8	383	6	ABU84287 Human sec
19	2044	96.8	383	6	ABR66161 Human sec
20	2044	96.8	383	6	ABR65551 Human sec
21	2044	96.8	383	6	ABU99491 Human sec
22	2044	96.8	383	6	ABU82730 Human PRO
23	2044	96.8	383	6	ABU89851 Novel hum
24	2044	96.8	383	6	ABU71491 Human PRO
25	2044	96.8	383	6	ABR68100 Human sec

26	2044	96.8	383	6	ABU96153	Abu96153 Novel hum
27	2044	96.8	383	6	ABU92584	Abu92584 Human sec
28	2044	96.8	383	6	ABO08661	ABO08661 Human sec
29	2044	96.8	383	6	ABO02713	ABO02713 Human sec
30	2044	96.8	383	6	ABR74867	ABR74867 Human sec
31	2044	96.8	383	6	ABR94629	ABR94629 Human sec
32	2044	96.8	383	6	ABU85602	ABU85602 Human PRO
33	2044	96.8	383	6	ABU98762	ABU98762 Novel hum
34	2044	96.8	383	6	ABU97977	ABU97977 Novel hum
35	2044	96.8	383	6	ABU91683	ABU91683 Novel hum
36	2044	96.8	383	6	ABU71937	ABU71937 Human sec
37	2044	96.8	383	6	ABU89376	ABU89376 Human PRO
38	2044	96.8	383	6	ABU86217	ABU86217 Human sec
39	2044	96.8	383	6	ABU67430	ABU67430 Human sec
40	2044	96.8	383	6	ABU80458	ABU80458 Human PRO
41	2044	96.8	383	6	ABO01820	ABO01820 Novel hum
42	2044	96.8	383	6	ABR99376	ABR99376 Human sec
43	2044	96.8	383	6	ABR98766	ABR98766 Human sec
44	2044	96.8	383	6	ABO16289	ABO16289 Human sec
45	2044	96.8	383	6	ABR92189	ABR92189 Human sec

ALIGNMENTS

RESULT 1
AAB48972
ID AAB48972 standard; protein; 392 AA.
XX
AC AAB48972;
XX
AC AAB48972;
DT 27-MAR-2001 (first entry).
XX
DE Human Zsig13 variant #1, SEQ ID NO:2.
XX
Human Zsig13; serine protease; chromosome 11q22.1; elastase homologue;
KW glutamyl endopeptidase homologue; factor X homologue; trypsin homologue;
KW trypsinogen homologue; mast cell protease homologue;
KW collagenase homologue; protein degradation; food processing; brewing;
KW alcohol production; laundry detergent component.
XX
Homo sapiens.
XX
US6153420-A.
PN
XX
PD 28-NOV-2000.
XX
PF 04-MAY-1998; 98US-00072384.
XX
PR 24-APR-1997; 97US-0044185P.
PR 17-APR-1998; 98US-00062142.
XX
(ZYMO) ZYMOGENETICS INC.
XX
Sheppard PO;
XX
WPI; 2001-060090/07.
DR N-PSDB; AAC91782.
XX
New isolated serine protease (designated Zsig13), useful in industrial processes to degrade unwanted proteins or alter the characteristics of protein-containing composition, as well as in industrial applications (e.g. brewing).
XX
Claim 1; Col 25-28; 26pp; English.
XX
The invention relates to human Zsig13 proteins (AAB48972-B48974), and to DNA encoding them (AAC91782-C91784). The invention also relates to expression vectors and host cells comprising a human Zsig13 DNA, and the recombinant production of a human Zsig13 protein or its precursor. Zsig13 is a serine protease, and has significant homology to Bacillus licheniformis glutamyl endopeptidase, human clotting factor X, human elastase, rat mast cell protease, Streptomyces griseus trypsin, bovine

CC trypsinogen, and Hypoderma lineatum collagenase. The gene encoding human
CC Zsig13 is located on chromosome 11q22.1. Zsig13 is useful in industrial
CC processes to degrade unwanted proteins or alter the characteristics of
CC protein-containing compositions. It may also be used in industrial
CC applications in which proteases are utilised, including food processing,
CC brewing and alcohol production, and as a component of a laundry
CC detergent. The present sequence represents a human Zsig13 variant
XX
SQ Sequence 392 AA;

Query Match 99.6%; Score 2104; DB 4; Length 392;
Best Local Similarity 100.0%; Pred. No. 4.6e-146; Mismatches 0; Indels 0; Gaps 0;
Matches 392; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MAGIPGLLFLFLFLLCAVGVSPYSAPWKPWPAYRLPVVLPQSTLNLAKEPFGAEAKLE 60
Db 1 MAGIPGLLFLFLFLLCAVGVSPYSAPWKPWPAYRLPVVLPQSTLNLAKEPFGAEAKLE 60
Qy 61 VSSSCGPQCHKGTPLPYTKAQLSYETLYANGSRTEKQVGIYILSSSGDGAXXRDSGS 120
Db 61 VSSSCGPQCHKGTPLPYTKAQLSYETLYANGSRTEKQVGIYILSSSGDGAXXRDSGS 120
Qy 121 SGKSRKRQIYGYDSRFSIFGKDFLLNYPSTSVKLSGTCTGLVAEXHVLTAACHIDG 180
Db 121 SGKSRKRQIYGYDSRFSIFGKDFLLNYPSTSVKLSGTCTGLVAEXHVLTAACHIDG 180
Qy 181 KTYVGTQKLRVGLFKPKFQKGGRGANDSTAMPQMKFQWIRVKTHTVPKGIKNAND 240
Db 181 KTYVGTQKLRVGLFKPKFQKGGRGANDSTAMPQMKFQWIRVKTHTVPKGIKNAND 240
Qy 241 IGMVDYALVELLKKPKHKKFPMKIGVSPPAKQLPGRIHFGSGYNDPRLGNLVYRFDVKDE 300
Db 241 IGMVDYALVELLKKPKHKKFPMKIGVSPPAKQLPGRIHFGSGYNDPRLGNLVYRFDVKDE 300
Qy 301 TYDLLYQCCDAQPGASGYGVYVVMKROQKWERKIIIGIFSGHQMVMNGSPQDFNVAVR 360
Db 301 TYDLLYQCCDAQPGASGYGVYVVMKROQKWERKIIIGIFSGHQMVMNGSPQDFNVAVR 360
Qy 361 ITPLKYAQCICWIKGNVLDCEGDTVFLPGSN 392
Db 361 ITPLKYAQCICWIKGNVLDCEGDTVFLPGSN 392

RESULT 2
AAB48973
ID AAB48973 standard; protein; 392 AA.
XX
AC AAB48973;
XX
DT 27-MAR-2001 (first entry)
XX
DE Human Zsig13 variant #2, SEQ ID NO:15.
XX
KW Human Zsig13; serine protease; chromosome 11q22.1; elastase homologue;
KW glutamyl endopeptidase homologue; factor X homologue; trypsin homologue;
KW trypsinogen homologue; mast cell protease homologue;
KW collagenase homologue; protein degradation; food processing; brewing;
KW alcohol production; laundry detergent component.
XX
OS Homo sapiens.
XX
FN US6153420-A.
XX
PD 28-NOV-2000.
XX
PF 04-MAY-1998; 98US-00072384.
XX
PR 24-APR-1997; 97US-0044185P.
PR 17-APR-1998; 98US-00062142.
XX
PA (ZYMO) ZYMOGENETICS INC.
XX
FI Sheppard PO;

XX WPI; 2001-060090/07.
DR N-PSDB; AAC91783.
XX
PT New isolated serine protease (designated Zsig13), useful in industrial
PT processes to degrade unwanted proteins or alter the characteristics of
PT protein-containing composition, as well as in industrial applications
PT (e.g. brewing).
XX
PS Claim 1; Col 35-38; 26pp; English.
XX
CC The invention relates to human Zsig13 proteins (AAB48972-B48974), and to
CC DNA encoding them (AAC91782-C91784). The invention also relates to
CC expression vectors and host cells comprising a human Zsig13 DNA, and the
CC recombinant production of a human Zsig13 protein or its precursor. Zsig13
CC is a serine protease, and has significant homology to Bacillus
CC licheniformis glutamyl endopeptidase, human clotting factor X, human
CC elastase, rat mast cell protease, Streptomyces griseus trypsin, bovine
CC trypsinogen, and Hypoderma lineatum collagenase. The gene encoding human
CC Zsig13 is located on chromosome 11q22.1. Zsig13 is useful in industrial
CC processes to degrade unwanted proteins or alter the characteristics of
CC protein-containing compositions. It may also be used in industrial
CC applications in which proteases are utilised, including food processing,
CC brewing and alcohol production, and as a component of a laundry
CC detergent. The present sequence represents a human Zsig13 variant
XX
SQ Sequence 392 AA;

Query Match 98.7%; Score 2085; DB 4; Length 392;
Best Local Similarity 98.2%; Pred. No. 1.1e-144;
Matches 385; Conservative 1; Mismatches 6; Indels 0; Gaps 0;
Qy 1 MAGIPGLLFLFLFLLCAVGVSPYSAPWKPWPAYRLPVVLPQSTLNLAKEPFGAEAKLE 60
Db 1 MAGIPGLLFLFLFLLCAVGVSPYSAPWKPWPAYRLPVVLPQSTLNLAKEPFGAEAKLE 60
Qy 61 VSSSCGPQCHKGTPLPYTKAQLSYETLYANGSRTEKQVGIYILSSSGDGAXXRDSGS 120
Db 61 VSSSCGPQCHKGTPLPYTKAQLSYETLYANGSRTEKQVGIYILSSSGDGAXXRDSGS 120
Qy 121 SGKSRKRQIYGYDSRFSIFGKDFLLNYPSTSVKLSGTCTGLVAEXHVLTAACHIDG 180
Db 121 SGKSRKRQIYGYDSRFSIFGKDFLLNYPSTSVKLSGTCTGLVAEXHVLTAACHIDG 180
Qy 181 KTYVGTQKLRVGLFKPKFQKGGRGANDSTAMPQMKFQWIRVKTHTVPKGIKNAND 240
Db 181 KTYVGTQKLRVGLFKPKFQKGGRGANDSTAMPQMKFQWIRVKTHTVPKGIKNAND 240
Qy 241 IGMVDYALVELLKKPKHKKFPMKIGVSPPAKQLPGRIHFGSGYNDPRLGNLVYRFDVKDE 300
Db 241 IGMVDYALVELLKKPKHKKFPMKIGVSPPAKQLPGRIHFGSGYNDPRLGNLVYRFDVKDE 300
Qy 301 TYDLLYQCCDAQPGASGYGVYVVMKROQKWERKIIIGIFSGHQMVMNGSPQDFNVAVR 360
Db 301 TYDLLYQCCDAQPGASGYGVYVVMKROQKWERKIIIGIFSGHQMVMNGSPQDFNVAVR 360
Qy 361 ITPLKYAQCICWIKGNVLDCEGDTVFLPGSN 392
Db 361 ITPLKYAQCICWIKGNVLDCEGDTVFLPGSN 392

RESULT 3
AAY08660
ID AAY08660 standard; protein; 383 AA.
XX
AC AAY08660;
XX
DT 09-AUG-1999 (first entry)
XX
DE W09927094 Seq ID 12.
XX
KW Transmembrane domain; human; nutrition; cytokine; cell differentiation;
KW immune stimulation; immune suppression; haematopoiesis; activin;

KW regulatory tissue growth; inhibitor; chemostatic; chemokinetic;
KW haemostatic; thrombolytic; tumour inhibitor; anti-inflammatory;
XX gene therapy; screening.

OS Homo sapiens.

XX WO9927094-A2.

XX 03-JUN-1999.

XX 20-NOV-1998; 98WO-JP005238.

XX 25-NOV-1997; 97JP-00323129.

XX (SAGA) SAGAMI CHEM RES CENT.

XX (PROT-) PROTEGENE INC.

XX Kato S, Kimura T, Sekine S;

XX WPI; 1999-357835/30.

XX Novel proteins containing transmembrane domains, useful as anti-inflammatory, immune stimulators/suppressors and tissue growth compounds.

XX Disclosure; Page 87-89; 89pp; English.

XX This invention describes novel human transmembrane containing proteins and their encoding nucleic acids. Although no specific use is given for the proteins, they may have a range of activities selected from nutritional uses, cytokine and cell differentiation, immune stimulation/suppression, haematopoiesis regulatory, tissue growth, activin/inhibin, chemostatic/chemokinetic, haemostatic/thrombolytic, receptor/ligand, tumour inhibitor, anti-inflammatory and other undefined activities. The cDNAs can be utilized as probes for gene diagnosis and as gene sources for gene therapy. The cDNAs can also be used for large scale expression of proteins. The transformed cells can be used for detection of the corresponding ligands and for screening of novel low-molecular pharmaceuticals

XX SQ Sequence 383 AA;

Query Match 96.8%; Score 2044; DB 2; Length 383;
Best Local Similarity 98.4%; Pred. No. 1.1e-141;
Matches 377; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 1 MAGIPGLLFLFLCAVGVSPYSAPWKTWPAYRLPVVLPSTLNLAKEPFGAEAKLE 60
DB 1 MAGIPGLLFLFLCAVGVSPYSAPWKTWPAYRLPVVLPSTLNLAKEPFGAEAKLE 60

QY 61 VSSSCGPGQCHKGTPPTPYEAKQYLSYETLYANGSRTEXQVGIYILSSSGDGAAXRDSGS 120
DB 61 VSSSCGPGQCHKGTPPTPYEAKQYLSYETLYANGSRTEXQVGIYILSSSGDGAAXRDSGS 120

QY 121 SGKSRKRQIYGYDSRFSIFGKDFLLNYPSTSVKLSCTGCTGLVAEXHVLTAACHIDG 180
DB 121 SGKSRKRQIYGYDSRFSIFGKDFLLNYPSTSVKLSCTGCTGLVAEXHVLTAACHIDG 180

QY 181 KTVVKGTKLRVGLFKPKFKDGRGANDSTAMPQMKFQIRKRVTHVPKGIKGNAND 240
DB 181 KTVVKGTKLRVGLFKPKFKDGRGANDSTAMPQMKFQIRKRVTHVPKGIKGNAND 240

QY 241 IGMDDYDYLLELKKPKHKKPMKMGVSPAPKQLPGGRIFHSGYDNDPGLNLYVFCVDKDE 300
DB 241 IGMDDYDYLLELKKPKHKKPMKMGVSPAPKQLPGGRIFHSGYDNDPGLNLYVFCVDKDE 300

QY 301 TYDLLVQCCDAQPCASGYGVYVWRKQKQKWERKIGIFSGHQTDMNGSPQDFNVAVR 360
DB 301 TYDLLVQCCDAQPCASGYGVYVWRKQKQKWERKIGIFSGHQTDMNGSPQDFNVAVR 360

QY 361 ITPKVAQICVWIKGNLYLDCREG 383
DB 361 ITPKVAQICVWIKGNLYLDCREG 383

RESULT 4

AA08657

ID RAY08657 standard; protein; 383 AA.

XX AC AAY08657;

XX DT 09-AUG-1999 (first entry)

XX Human transmembrane domain containing protein from clone HP10493.

XX Transmembrane domain; human; nutrition; cytokine; cell differentiation; immune stimulation; immune suppression; haematopoiesis; activin; regulatory tissue growth; inhibitor; chemostatic; chemokinetic; haemostatic; thrombolytic; tumour inhibitor; anti-inflammatory; gene therapy; screening.

XX Homo sapiens.

XX WO9927094-A2.

XX 03-JUN-1999.

XX 20-NOV-1998; 98WO-JP005238.

XX 25-NOV-1997; 97JP-00323129.

XX (SAGA) SAGAMI CHEM RES CENT.

XX (PROT-) PROTEGENE INC.

XX Kato S, Kimura T, Sekine S;

XX WPI; 1999-357835/30.

XX N-PSDB; AAX77690, AAX77691.

XX Novel proteins containing transmembrane domains, useful as anti-inflammatory, immune stimulators/suppressors and tissue growth compounds.

XX Claim 1; Page 68-69; 89pp; English.

XX This invention describes novel human transmembrane containing proteins and their encoding nucleic acids. Although no specific use is given for the proteins, they may have a range of activities selected from nutritional uses, cytokine and cell differentiation, immune stimulation/suppression, haematopoiesis regulatory, tissue growth, activin/inhibin, chemostatic/chemokinetic, haemostatic/thrombolytic, receptor/ligand, tumour inhibitor, anti-inflammatory and other undefined activities. The cDNAs can be utilized as probes for gene diagnosis and as gene sources for gene therapy. The cDNAs can also be used for large scale expression of proteins. The transformed cells can be used for detection of the corresponding ligands and for screening of novel low-molecular pharmaceuticals

XX SQ Sequence 383 AA;

Query Match 96.8%; Score 2044; DB 2; Length 383;
Best Local Similarity 98.4%; Pred. No. 1.1e-141;
Matches 377; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 1 MAGIPGLLFLFLCAVGVSPYSAPWKTWPAYRLPVVLPSTLNLAKEPFGAEAKLE 60
DB 1 MAGIPGLLFLFLCAVGVSPYSAPWKTWPAYRLPVVLPSTLNLAKEPFGAEAKLE 60

QY 61 VSSSCGPGQCHKGTPPTPYEAKQYLSYETLYANGSRTEXQVGIYILSSSGDGAAXRDSGS 120
DB 61 VSSSCGPGQCHKGTPPTPYEAKQYLSYETLYANGSRTEXQVGIYILSSSGDGAAXRDSGS 120

QY 121 SGKSRKRQIYGYDSRFSIFGKDFLLNYPSTSVKLSCTGCTGLVAEXHVLTAACHIDG 180
DB 121 SGKSRKRQIYGYDSRFSIFGKDFLLNYPSTSVKLSCTGCTGLVAEXHVLTAACHIDG 180

QY 181 KTVYKGTQKLRVGLKPKFKDGGGRANDSTSAMPEQMKFQWIRVKTTHVPGWIKGNAND 240
 Db 181 KTVYKGTQKLRVGLKPKFKDGGGRANDSTSAMPEQMKFQWIRVKTTHVPGWIKGNAND 240
 QY 241 IGMDDYDVALLELKKPKRKFVKMGIVSPPAKQLPGGRIFHSGYDNDPFGNLVYRFGCDVKDE 300
 Db 241 IGMDDYDVALLELKKPKRKFVKMGIVSPPAKQLPGGRIFHSGYDNDPFGNLVYRFGCDVKDE 300
 QY 301 TYDLLYQCCDAQPGASGSGYVYVMWKRQOQKWERKIIGIPSGHQMVDMMGSPQDFNVAVR 360
 Db 301 TYDLLYQCCDAQPGASGSGYVYVMWKRQOQKWERKIIGIPSGHQMVDMMGSPQDFNVAVR 360
 QY 361 ITPKVAQICWIKGNVLDREG 383
 Db 361 ITPKVAQICWIKGNVLDREG 383
 RESULT 5
 ID AAY13390 standard; protein; 383 AA.
 AC AAY13390;
 XX
 XX 25-JUN-1999 (first entry)
 XX
 DE Amino acid sequence of protein PRO307.
 XX
 KW Secreted protein; transmembrane protein; human; enterocolitis;
 KW Zollinger-Ellison syndrome; gastrointestinal ulceration;
 KW congenital microvillus atrophy; skin disease; cell growth;
 KW abnormal keratinocyte differentiation; psoriasis; epithelial cancer;
 KW Parkinson's disease; Alzheimer's disease; ALS; neuropathy; fibromodulin;
 KW dermal scarring; Usher Syndrome; Atrophia areata; anti-thrombotic;
 KW wound healing; tissue repair.
 XX
 OS Homo sapiens.
 XX
 XX WO9914328-A2..
 XX
 PD 25-MAR-1999.
 XX
 PF 16-SEP-1998; 98WO-US019330.
 XX
 PR 17-SEP-1997; 97US-0059113P.
 PR 17-SEP-1997; 97US-0059115P.
 PR 17-SEP-1997; 97US-0059117P.
 PR 17-SEP-1997; 97US-0059119P.
 PR 17-SEP-1997; 97US-0059121P.
 PR 17-SEP-1997; 97US-0059122P.
 PR 17-SEP-1997; 97US-0059184P.
 PR 18-SEP-1997; 97US-0059263P.
 PR 18-SEP-1997; 97US-0059266P.
 PR 18-SEP-1997; 97US-0062125P.
 PR 17-OCT-1997; 97US-0062285P.
 PR 17-OCT-1997; 97US-0062287P.
 PR 17-OCT-1997; 97US-0062287P.
 PR 21-OCT-1997; 97US-0063486P.
 PR 24-OCT-1997; 97US-0062814P.
 PR 24-OCT-1997; 97US-0062816P.
 PR 24-OCT-1997; 97US-0063045P.
 PR 24-OCT-1997; 97US-0063120P.
 PR 24-OCT-1997; 97US-0063121P.
 PR 24-OCT-1997; 97US-0063127P.
 PR 24-OCT-1997; 97US-0063128P.
 PR 27-OCT-1997; 97US-0063327P.
 PR 27-OCT-1997; 97US-0063329P.
 PR 28-OCT-1997; 97US-0063341P.
 PR 28-OCT-1997; 97US-0063342P.
 PR 28-OCT-1997; 97US-0063344P.
 PR 28-OCT-1997; 97US-0063349P.
 PR 28-OCT-1997; 97US-0063549P.
 PR 28-OCT-1997; 97US-0063564P.
 PR 28-OCT-1997; 97US-0063435P.
 PR 29-OCT-1997; 97US-0063704P.

PR 29-OCT-1997; 97US-0063732P.
 PR 29-OCT-1997; 97US-0063734P.
 PR 29-OCT-1997; 97US-0063735P.
 PR 29-OCT-1997; 97US-0063738P.
 PR 29-OCT-1997; 97US-0064215P.
 PR 31-OCT-1997; 97US-0063870P.
 PR 31-OCT-1997; 97US-0064103P.
 PR 03-NOV-1997; 97US-0064248P.
 PR 07-NOV-1997; 97US-0064809P.
 PR 12-NOV-1997; 97US-0065186P.
 PR 17-NOV-1997; 97US-0065846P.
 PR 18-NOV-1997; 97US-0065693P.
 PR 21-NOV-1997; 97US-0066120P.
 PR 21-NOV-1997; 97US-0066364P.
 PR 24-NOV-1997; 97US-0066453P.
 PR 24-NOV-1997; 97US-0066466P.
 PR 24-NOV-1997; 97US-0066511P.
 PR 24-NOV-1997; 97US-0066770P.
 PR 24-NOV-1997; 97US-0066772P.
 PR 25-NOV-1997; 97US-0066840P.
 XX
 PA (GETH) GENENTECH INC.
 XX
 XX Wood WI, Gurney AL, Goddard A, Pennica D, Chen J, Yuan J;
 PI WPI; 1999-229533/19.
 XX N-PSDB; AAX52261.
 DR
 DR New isolated human genes and polypeptides used in, e.g. treatment of
 PT gastrointestinal ulceration.
 PT
 XX Claim 12; Fig 96; 320pp; English.
 XX
 CC AAY13344-403 represent secreted and transmembrane human proteins. The
 CC cDNA sequences are obtained from cDNA libraries, prepared from fetal
 CC lung, fetal kidney, fetal brain, fetal liver and fetal retina. The
 CC encoded polypeptides have specific uses based on their homology to known
 CC polypeptides, e.g. PRO211 and PRO217 can be used for disorders associated
 CC with the preservation and maintenance of gastrointestinal mucosa and the
 CC repair of acute and chronic mucosal lesions (e.g. enterocolitis,
 CC Zollinger-Ellison syndrome, gastrointestinal ulceration and congenital
 CC microvillus atrophy), skin diseases associated with abnormal keratinocyte
 CC differentiation (e.g. psoriasis, epithelial cancers such as lung squamous
 CC cell carcinoma of the vulva and gliomas), potent effects on cell growth
 CC and development, diseases related to growth or survival of nerve cells
 CC including Parkinson's disease, Alzheimer's disease, ALS, neuropathies or
 CC cancer. PRO265 can be used as for fibromodulin, e.g. for reducing dermal
 CC scarring. PRO264 can be used as a target for anti-tumor drugs. PRO533 may
 CC be used in the treatment of Usher Syndrome or Atrophia areata; PRO269 can
 CC be used as an anti-thrombotic agent; PRO287 polypeptides and portions may
 CC have therapeutic applications in wound healing and tissue repair; PRO317
 CC can be used for treating problems of the kidney, uterus, endometrium,
 CC blood vessels, or related tissue, e.g. in the heart of genital tract
 XX
 SQ Sequence 383 AA;
 Query Match 96.8%; Score 2044; DB 2; Length 383;
 Best Local Similarity 98.4%; Pred. No. 1.1e-141;
 Matches 377; Conservative 1; Mismatches 5; Indels 0; Gaps 0;
 QY 1 MAGIFGLLFLFFLLCAVQGVSPYSAPKMTWPAYRLPVLPQSTLNLAKEPFGAEAKLE 60
 Db 1 MAGIFGLLFLFFLLCAVQGVSPYSAPKMTWPAYRLPVLPQSTLNLAKEPFGAEAKLE 60
 QY 61 VSSSCGPGCHKGTPLPTTYKEAKQYLSYETLYANGSRTEXQVIGIYILSSGDCAXXRDSSG 120
 Db 61 VSSSCGPGCHKGTPLPTTYKEAKQYLSYETLYANGSRTEXQVIGIYILSSGDCAXXRDSSG 120
 QY 121 SGKSRKQIYGYDSRFSIFGKDFLLNYPFSTSVKLSGTCTGLVAEXHVLTAACHIDHG 180
 Db 121 SGKSRKQIYGYDSRFSIFGKDFLLNYPFSTSVKLSGTCTGLVAEXHVLTAACHIDHG 180
 QY 181 KTVYKGTQKLRVGLKPKFKDGGGRANDSTSAMPEQMKFQWIRVKTTHVPGWIKGNAND 240

Db 181 KTVVGTQKLRVGLFKPKFGDGRGANDSTAMPEQMKFQWIRKTHVPKGIKGNAND 240
 Qy 241 IGDYDVALLELKKPKKFKPMKIGVSPAKQLPGRIHFSGYNDPRGNLYVRFCDVKDE 300
 Db 241 IGDYDVALLELKKPKKFKPMKIGVSPAKQLPGRIHFSGYNDPRGNLYVRFCDVKDE 300
 Qy 301 TYDLLYQCDQAQPGASGYGVYVVMWKRQKQKWKRIIGIFSGHQWVDMNGSPQDFNVAVR 360
 Db 301 TYDLLYQCDQAQPGASGYGVYVVMWKRQKQKWKRIIGIFSGHQWVDMNGSPQDFNVAVR 360
 Qy 361 ITPLKYAQICYNKGNLYDCREG 383
 Db 361 ITPLKYAQICYNKGNLYDCREG 383

RESULT 6

AAV88277
 ID AAY88277 standard; protein; 383 AA.

AC AAY88277;

XX 16-OCT-2000 (first entry)

DT Human TANGO 186 protein.

DE TANGO 180; TANGO 181; TANGO 182; TANGO 183; TANGO 184; TANGO 185;

XX TANGO 186; TANGO 188; TANGO 189; TANGO 215; TANGO 187; human; murine;

KW secreted protein; transmembrane protein; gene therapy; vaccine;

KW diagnosis; treatment; detection.

XX Homo sapiens.

XX WO200018904-A2.

XX 06-APR-2000.

XX 30-SEP-1999; 99WO-US022817.

XX 30-SEP-1998; 98US-00164220.

PR 02-OCT-1998; 98US-00164169.

XX (MILL-) MILLENNIUM BIOTHERAPEUTICS INC.

XX Barnes TW;

XX WPI; 2000-293144/25.

DR N-PSDB; AAA39945, AAA39946.

XX Isolated nucleic acids encoding TANGO polypeptides useful for preventing,

PT diagnosing and treating diseases associated with inappropriate protein

PT expression.

XX Claim 9; Fig 13; 249pp; English.

PS This invention describes novel human and murine nucleic acids encoding
 CC TANGO polypeptides (which are either wholly secreted or transmembrane
 CC proteins) which can be used for gene therapy and/or vaccination. The
 CC peptides are designated TANGO 180 to TANGO 189 and TANGO 215. The nucleic
 CC acids may be used to produce TANGO 180 to TANGO 189 and TANGO 215
 CC polypeptides according to standard recombinant DNA methodologies. They
 CC may also be used to detect and quantify the presence of TANGO nucleic
 CC acids in a sample and therefore identify or diagnose diseases associated
 CC with inappropriate TANGO expression (e.g. diseases related to over or
 CC under expression of the polypeptides or the expression of inactive
 CC polypeptides). The nucleic acids and the polypeptides they encode may be
 CC used according to standard gene therapy protocols, to treat diseases
 CC associated with inappropriate TANGO expression by supplementing a
 CC patient's own production of the polypeptide or to rectify mutations that
 CC may result in expression of an abnormally active polypeptide. The
 CC polypeptides may also be used to identify and produce agonists and
 CC antagonists of TANGO expression and activity which may be used to
 CC modulate TANGO related processes and diseases. The polypeptides are

CC particularly useful for use as antigens for producing antibodies to TANGO
 CC proteins which may be used for inhibiting the activity of TANGO proteins.
 CC They may also be used to detect and quantify the presence of TANGO
 CC proteins in samples and therefore identify patients in whom the protein
 CC is over- or under-expressed. This sequence represents the human TANGO 186
 CC protein described in the method of the invention

XX SQ Sequence 383 AA;

Query Match 96.8%; Score 2044; DB 3; Length 383;

Best Local Similarity 98.4%; Pred. No. 1.le-141;

Matches 377; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

Qy 1 MAGIPGLLFLFLCAVGVSPYSAPWKPPTPAYRLPVVLPSTLNLAKEPFGASAKLE 60

Db 1 MAGIPGLLFLFLCAVGVSPYSAPWKPPTPAYRLPVVLPSTLNLAKEPFGASAKLE 60

Qy 61 VSSSCGPGCHKGTPLPTTKEAKQYLSYETLYANGSRTEXQVGIYIILSSGSGAXRDSGS 120

Db 61 VSSSCGPGCHKGTPLPTTKEAKQYLSYETLYANGSRTEXQVGIYIILSSGSGAXRDSGS 120

Qy 121 SGKSRKRQIYGYDSRFSIFGKDFLLNYPFSTSVKLTGCTGTLVAEKHVLTAAHCIDHG 180

Db 121 SGKSRKRQIYGYDSRFSIFGKDFLLNYPFSTSVKLTGCTGTLVAEKHVLTAAHCIDHG 180

Qy 181 KTVVGTQKLRVGLFKPKFGDGRGANDSTAMPEQMKFQWIRKTHVPKGIKGNAND 240

Db 181 KTVVGTQKLRVGLFKPKFGDGRGANDSTAMPEQMKFQWIRKTHVPKGIKGNAND 240

Qy 241 IGDYDVALLELKKPKKFKPMKIGVSPAKQLPGRIHFSGYNDPRGNLYVRFCDVKDE 300

Db 241 IGDYDVALLELKKPKKFKPMKIGVSPAKQLPGRIHFSGYNDPRGNLYVRFCDVKDE 300

Qy 301 TYDLLYQCDQAQPGASGYGVYVVMWKRQKQKWKRIIGIFSGHQWVDMNGSPQDFNVAVR 360

Db 301 TYDLLYQCDQAQPGASGYGVYVVMWKRQKQKWKRIIGIFSGHQWVDMNGSPQDFNVAVR 360

Qy 361 ITPLKYAQICYNKGNLYDCREG 383

Db 361 ITPLKYAQICYNKGNLYDCREG 383

RESULT 7

AAV87270

ID AAY87270 standard; protein; 383 AA.

XX AAY87270;

XX 11-MAY-2000 (first entry)

XX Human signal peptide containing protein HSP-47 SEQ ID NO:47.

XX Human; signal peptide-containing protein; HSP-47; diagnosis; cancer;

KW inflammation; cardiovascular disease; anticancer; anti-inflammatory;

KW antimicrobial; neurotropic; neuroprotective; cardiovascular; hepatotropic;

KW antitastmatic; gene therapy; cell proliferation; neurological disorder;

KW reproductive disorder; developmental disorder; arteriosclerosis;

KW cirrhosis; psoriasis; acquired immune deficiency syndrome; anaemia;

KW asthma; Crohn's disease; infection; Alzheimer's disease; schizophrenia;

KW Parkinson's disease; Huntington's disease; ovulatory defect;

KW muscular dystrophy.

XX Homo sapiens.

OS WO200000610-A2.

PN 06-JAN-2000.

PD 25-JUN-1999; 99WO-US014484.

PF 26-JUN-1998; 98US-0090762P.

PR 31-JUL-1998; 98US-0094983P.

PR 01-OCT-1998; 98US-0102686P.

CC and ulcers, to induce cartilage and/or bone growth in circumstances where
 CC bone is not normally formed and thus have an application in healing bone
 CC fractures and cartilage damage or defects, prophylactic use in fracture
 CC reduction and also in the improved fixation of artificial joints
 XX SQ Sequence 383 AA;

Query Match 96.8%; Score 2044; DB 3; Length 383;
 Best Local Similarity 98.4%; Pred. No. 1.1e-141;
 Matches 377; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

Qy 1 MAGIPGLLFLFLCAVGVSPYSAPWKTWPAYRLPVVLPSTLNLAKEPFGAEAKLE 60
 Db 1 MAGIPGLLFLFLCAVGVSPYSAPWKTWPAYRLPVVLPSTLNLAKEPFGAEAKLE 60
 Qy 61 VSSSCGPGQCHGTPLPTPYEAKQVLSYETLYANGSRTEKQVGIYILSSSGDGAAXRDSGS 120
 Db 61 VSSSCGPGQCHGTPLPTPYEAKQVLSYETLYANGSRTEKQVGIYILSSSGDGAAXRDSGS 120
 Qy 121 SGKSRKROIYGYDSRFSIFGKDFLLNYPSTSVKLSGTCTGLVAEXHVLTAACHIDG 180
 Db 121 SGKSRKROIYGYDSRFSIFGKDFLLNYPSTSVKLSGTCTGLVAEXHVLTAACHIDG 180
 Qy 181 KTVVGTQKLRVGLFKPKFDCGGRANDSTSAMPEQMKFQWIRKRVTHVPKGIKGNAND 240
 Db 181 KTVVGTQKLRVGLFKPKFDCGGRANDSTSAMPEQMKFQWIRKRVTHVPKGIKGNAND 240
 Qy 241 IGMVDYDYLLELKKPKHKKFPMKIGVSPAPKQLPGRIFHSGYDNDPGLNLYRFDCKDE 300
 Db 241 IGMVDYDYLLELKKPKHKKFPMKIGVSPAPKQLPGRIFHSGYDNDPGLNLYRFDCKDE 300
 Qy 301 TYDILLYQCCDAQPGASGYGVYVMWKRQOQKWERKIIGIFSGHQWDMNGSPQDFNVAVR 360
 Db 301 TYDILLYQCCDAQPGASGYGVYVMWKRQOQKWERKIIGIFSGHQWDMNGSPQDFNVAVR 360
 Qy 361 ITPLKYAQICYWKGNLYDCREG 383
 Db 361 ITPLKYAQICYWKGNLYDCREG 383

RESULT 9
 AAB25618
 ID AAB25618 standard; protein; 383 AA.
 XX AAB25618;
 AC
 XX
 DT 21-NOV-2000 (first entry)
 XX
 DE Protein encoded by human secreted protein gene #10.
 XX
 KW Secreted protein; immunosuppressant; anti-inflammatory; antiarthritic;
 KW antirheumatic, dermatological; antiproliferative; antiarteriosclerotic;
 KW anticancer; vulnary; antiviral; antibacterial; antifungal;
 KW immune disorder; Addison's disease; rheumatoid arthritis; dermatitis;
 KW multiple sclerosis; inflammatory disorder; inflammatory bowel disease;
 KW Crohn's disease; nephritis; hyperproliferative disorder;
 KW cardiovascular disorder; coronary arteriosclerosis; myocarditis; cancer;
 KW melanoma; lymphoma; wound healing; human; chromosome 12.
 XX
 OS Homo sapiens.
 XX
 PN WO200029435-A1.
 XX
 PD 25-MAY-2000.
 XX
 PF 27-OCT-1999; 99WO-US025031.
 XX
 PR 28-OCT-1998; 98US-0105971P.
 XX
 PA (HUMA-) HUMAN GENOME SCI INC.
 XX
 PI Ni J, Ruben SM, Olsen HS, Young PE, Kenny JJ, Moore PA, Wei Y;
 PI Greene JM;

XX WPI; 2000-387742/33.
 DR
 XX
 PT Isolated nucleic acid molecules encoding human secreted proteins are used
 PT for the prevention, amelioration and treatment of autoimmune,
 PT inflammatory, hyperproliferative and cardiovascular disorders, cancer,
 PT wounds, and infectious diseases.
 XX
 PS Disclosure; Page 169; 803pp; English.
 XX

CC The present invention relates to 12 secreted human proteins and the
 CC nucleotide sequences encoding them. The polynucleotide sequences given in
 CC AAA80606-A80623 encode the 12 secreted protein sequences given in
 CC AAB25576-B25593. The human secreted proteins have various activities
 CC dependent on the tissues in which they are expressed. Examples of the
 CC activities of the proteins include: immunosuppressant; anti-inflammatory;
 CC antiarthritic; antirheumatic, dermatological; antiproliferative;
 CC antiarteriosclerotic; anticancer; vulnary; antiviral; antibacterial;
 CC and antifungal activity. The proteins, polypeptides, agonists and
 CC antagonists may be used to treat prevent and/or diagnose various disease,
 CC disorders and conditions examples of which include: immune disorders e.g.
 CC Addison's disease, rheumatoid arthritis, dermatitis, and multiple
 CC sclerosis; inflammatory disorders e.g. inflammatory bowel disease,
 CC Crohn's disease and nephritis; hyperproliferative disorders such as
 CC paraproteinemias and purpura; cardiovascular disorders e.g. coronary
 CC arteriosclerosis and myocarditis; cancer e.g. melanoma and lymphoma. The
 CC proteins and polynucleotide sequences may also be used in wound healing
 CC and the treatment of infectious diseases. The human secreted protein gene
 CC #10 and protein sequences are represented in sequences AAA80615 and
 CC AAB25585. Secreted protein gene #10 is located on chromosome 12.
 CC Sequences AAB25616-B25618 represent alternative secreted protein #10
 CC sequences and AAA80609-A80676 represent genes which are related to the
 CC secreted protein gene#10
 XX

SQ Sequence 383 AA;

Query Match 96.8%; Score 2044; DB 3; Length 383;
 Best Local Similarity 98.4%; Pred. No. 1.1e-141;
 Matches 377; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

Qy 1 MAGIPGLLFLFLCAVGVSPYSAPWKTWPAYRLPVVLPSTLNLAKEPFGAEAKLE 60
 Db 1 MAGIPGLLFLFLCAVGVSPYSAPWKTWPAYRLPVVLPSTLNLAKEPFGAEAKLE 60
 Qy 61 VSSSCGPGQCHGTPLPTPYEAKQVLSYETLYANGSRTEKQVGIYILSSSGDGAAXRDSGS 120
 Db 61 VSSSCGPGQCHGTPLPTPYEAKQVLSYETLYANGSRTEKQVGIYILSSSGDGAAXRDSGS 120
 Qy 121 SGKSRKROIYGYDSRFSIFGKDFLLNYPSTSVKLSGTCTGLVAEXHVLTAACHIDG 180
 Db 121 SGKSRKROIYGYDSRFSIFGKDFLLNYPSTSVKLSGTCTGLVAEXHVLTAACHIDG 180
 Qy 181 KTVVGTQKLRVGLFKPKFDCGGRANDSTSAMPEQMKFQWIRKRVTHVPKGIKGNAND 240
 Db 181 KTVVGTQKLRVGLFKPKFDCGGRANDSTSAMPEQMKFQWIRKRVTHVPKGIKGNAND 240
 Qy 241 IGMVDYDYLLELKKPKHKKFPMKIGVSPAPKQLPGRIFHSGYDNDPGLNLYRFDCKDE 300
 Db 241 IGMVDYDYLLELKKPKHKKFPMKIGVSPAPKQLPGRIFHSGYDNDPGLNLYRFDCKDE 300
 Qy 301 TYDILLYQCCDAQPGASGYGVYVMWKRQOQKWERKIIGIFSGHQWDMNGSPQDFNVAVR 360
 Db 301 TYDILLYQCCDAQPGASGYGVYVMWKRQOQKWERKIIGIFSGHQWDMNGSPQDFNVAVR 360
 Qy 361 ITPLKYAQICYWKGNLYDCREG 383
 Db 361 ITPLKYAQICYWKGNLYDCREG 383

RESULT 10
 AAB25592
 ID AAB25592 standard; protein; 383 AA.
 XX

AC AAB25592;
 XX DT 21-NOV-2000 (first entry)
 XX DE Protein encoded by human secreted protein gene #10 clone HUSQ05.
 XX KW Secreted protein; immunosuppressant; anti-inflammatory; antiarthritic;
 KW antihemetic, dermatological; antiproliferative; antiarthritic;
 KW anticancer; vulnary; antiviral; antibacterial; antifungal;
 KW immune disorder; Addison's disease; rheumatoid arthritis; dermatitis;
 KW multiple sclerosis; inflammatory disorder; inflammatory bowel disease;
 KW Crohn's disease; nephritis; hyperproliferative disorder;
 KW cardiovascular disorder; coronary arteriosclerosis; myocarditis; cancer;
 KW melanoma; lymphoma; wound healing; human; chromosome 12.
 XX OS Homo sapiens.
 XX PN W0200029435-A1.
 XX PD 25-MAY-2000.
 XX PF 27-OCT-1999; 99WO-US025031.
 XX PR 28-OCT-1998; 98US-0105971P.
 XX PA (HUMA-) HUMAN GENOME SCI INC.
 XX PI Ni J, Ruben SM, Olsen HS, Young PE, Kenny JJ, Moore PA, Wei Y;
 PI Greene JM;
 XX WPI; 2000-387742/33.
 XX Isolated nucleic acid molecules encoding human secreted proteins are used
 XX for the prevention, amelioration and treatment of autoimmune,
 XX inflammatory, hyperproliferative and cardiovascular disorders, cancer,
 XX wounds, and infectious diseases.
 XX Claim 1; Page 684-685; 803pp; English.
 XX The present invention relates to 12 secreted human proteins and the
 XX nucleotide sequences encoding them. The polynucleotide sequences given in
 CC AAA80606-A80623 encode the 12 secreted protein sequences given in
 CC AAB25576-B25593. The human secreted proteins have various activities
 CC dependent on the tissues in which they are expressed. Examples of the
 CC activities of the proteins include: immunosuppressant; anti-inflammatory;
 CC antiarthritic; antirheumatic; dermatological; antiproliferative;
 CC antidiabetic; anticancer; vulnary; antiviral; antibacterial;
 CC and antifungal activity. The proteins, polypeptides, agonists and
 CC antagonists may be used to treat prevent and/or diagnose various disease,
 CC disorders and conditions examples of which include: immune disorders e.g.
 CC Addison's disease, rheumatoid arthritis, dermatitis, and multiple
 CC sclerosis; inflammatory disorders e.g. inflammatory bowel disease,
 CC Crohn's disease and nephritis; hyperproliferative disorders such as
 CC paraproteinemias and purpura; cardiovascular disorders e.g. coronary
 CC arteriosclerosis and myocarditis; cancer e.g. melanoma and lymphoma. The
 CC proteins and polynucleotide sequences may also be used in wound healing
 CC and the treatment of infectious diseases. The human secreted protein gene
 CC #10 and protein sequences are represented in sequences AAA80615 and
 CC AAB25585. Secreted protein gene #10 is located on chromosome 12.
 CC Sequences AAB25616-B25618 represent alternative secreted protein #10
 CC sequences and AAA80669-A80676 represent genes which are related to the
 CC secreted protein gene#10
 XX Sequence 383 AA;
 Query Match 96.8%; Score 2044; DB 3; Length 383;
 Best Local Similarity 98.4%; Pred. No. 1.1e-141;
 Matches 377; Conservative 1; Mismatches 5; Indels 0; Gaps 0;
 QY 1 MAGIPGLLFLFLLCAGVGQSPYSAPWKPYPAYRLPVVLPGSTNLAKPFGAAKLE 60
 DB 1 MAGIPGLLFLFLLCAGVGQSPYSAPWKPYPAYRLPVVLPGSTNLAKPFGAAKLE 60

QY 61 VSSCGPQCHKGTPLPTYKAKOYLSYETLYANGSRTEKXQVGIYILSSSGDGAXXRDSGS 120
 DB |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||: 120
 QY 121 SKSRRKQIYGVDSRFISFGKDFLLNYPFSTSVKLSGTCTGLVAEXHVLTAACHIDG 180
 DB |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||: 180
 QY 121 SKSRRKQIYGVDSRFISFGKDFLLNYPFSTSVKLSGTCTGLVAEXHVLTAACHIDG 180
 DB |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||: 180
 QY 181 KTYVKGTKLVRGFLKPKFKDGGRGANDSTAMPQMKFQWIRVKTHTVPGWKIGNAND 240
 DB |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||: 240
 QY 181 KTYVKGTKLVRGFLKPKFKDGGRGANDSTAMPQMKFQWIRVKTHTVPGWKIGNAND 240
 DB |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||: 240
 QY 241 IGMVDYDYLLELKKPKFKMKGIVSPPAKQIIPGRIHFGSYDNDPGLNVRFCVDKDE 300
 DB |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||: 300
 QY 241 IGMVDYDYLLELKKPKFKMKGIVSPPAKQIIPGRIHFGSYDNDPGLNVRFCVDKDE 300
 DB |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||: 300
 QY 301 TYDLLYQQCDAOPGASGVGVYVMKROQKWKRIIGIFSGHQWYDMNGSPQDFNVAVR 360
 DB |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||: 360
 QY 301 TYDLLYQQCDAOPGASGVGVYVMKROQKWKRIIGIFSGHQWYDMNGSPQDFNVAVR 360
 DB |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||: 360
 QY 361 ITPLKYAQICYWIKGNLYLDCREG 383
 DB |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||: 383
 QY 361 ITPLKYAQICYWIKGNLYLDCREG 383
 DB |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||: 383
 RESULT 11
 ADC78573
 ID ADC78573 standard; protein; 383 AA.
 XX AC ADC78573;
 XX DT 01-JAN-2004 (first entry)
 XX DE Human PRO307 protein.
 XX KW antinflammatory; antiulcer; cytostatic; antipsoriatic; antiparkinsonian;
 KW neurotrophic; osteopathic; antiasthmatic; antiarthritic; antirheumatic;
 KW antidiabetic; cardiatic; antidiabetic; cerebroprotective;
 KW thrombolytic; immunomodulator; enterocolitis; Zollinger-Ellison syndrome;
 KW gastrointestinal ulceration; psoriasis; cancer; Parkinson's disease;
 KW Alzheimer's; ALS; neuropathy; dermal scarring; wound healing;
 KW nerve repair; thrombosis; bone; cartilage formation; angiogenesis;
 KW asthma; rheumatoid arthritis; multiple sclerosis; inflammatory disorder;
 KW atherosclerosis; cardiac injury; infertility; premature aging; AIDS;
 KW diabetes; stroke; gene therapy; transgenic; PRO; human.
 XX OS Homo sapiens.
 XX WO200015796-A2.
 XX 23-MAR-2000.
 XX 15-SEP-1999; 99WO-US021090.
 XX 16-SEP-1998; 98WO-US019330.
 XX (GETH) GENENTECH INC.
 XX Chen J, Goddard A, Gurney AL, Hillan K, Pennica D, Wood WI;
 XX Yuan J;
 XX WPI; 2000-271434/23.
 XX N-PSDB; ADC78572.
 XX Novel nucleic acids encoding secreted and transmembrane polypeptides with
 XX homology, e.g. to growth and cancer-associated antigens.
 XX Claim 12; SEQ ID NO 261; 355pp; English.
 XX The invention relates to a novel nucleic acid encoding a PRO polypeptide.
 CC The polypeptides and polynucleotides of the invention may be useful as
 CC research tools and as therapeutics for treating enterocolitis, Zollinger-

CC Ellison syndrome, gastrointestinal ulceration, psoriasis, cancer,
 CC Parkinson's disease, Alzheimer's disease, ALS, neuropathies, dermal
 CC scarring and wound healing, nerve repair, thrombosis, bone and/or
 CC cartilage formation, angiogenesis, asthma, rheumatoid arthritis, multiple
 CC sclerosis, inflammatory disorders, atherosclerosis, cardiac injury,
 CC infertility, premature aging, AIDS, diabetes complications and stroke.
 CC The molecules may also be utilised during gene therapy procedures and
 CC transgenic animal production. The current sequence is that of the human
 CC PRO protein of the invention.
 XX
 SQ Sequence 383 AA;
 Query Match 96.8%; Score 2044; DB 3; Length 383;
 Best Local Similarity 98.4%; Pred. No. 1.1e-141;
 Matches 377; Conservative 1; Mismatches 5; Indels 0; Gaps 0;
 QY 1 MAGIPGLLFLFLCAVGVSPYSAPWKPTWPAYRLPVVLPQSTLNLAKEPFGAEAKLE 60
 DB 1 MAGIPGLLFLFLCAVGVSPYSAPWKPTWPAYRLPVVLPQSTLNLAKEPFGAEAKLE 60
 QY 61 VSSSCGPOCHKGTPLPTYPEAKQYLSYETLYANGSRTEQVGIYILSSGDXAXRDSGS 120
 DB 61 VSSSCGPOCHKGTPLPTYPEAKQYLSYETLYANGSRTEQVGIYILSSGDXAXRDSGS 120
 QY 121 SGSRKRQIYGYDSRFSIFGKDFLLNYPSTSVKLSGTCTGLVAEXHVLTAACHIDG 180
 DB 121 SGSRKRQIYGYDSRFSIFGKDFLLNYPSTSVKLSGTCTGLVAEXHVLTAACHIDG 180
 QY 181 KTYVKGQKLRVGLFKPKFQDGGGRANDSTSAMPEQMKFQWIRKTHVPKGIKGNAND 240
 DB 181 KTYVKGQKLRVGLFKPKFQDGGGRANDSTSAMPEQMKFQWIRKTHVPKGIKGNAND 240
 QY 241 IGMVDYALLELKKPHKPKMKIGVSPPAKQIPGRIHFSGYDNDPQNLVYRFDVKDE 300
 DB 241 IGMVDYALLELKKPHKPKMKIGVSPPAKQIPGRIHFSGYDNDPQNLVYRFDVKDE 300
 QY 301 TYDLLYQCCDAQPGASGVYVVRMKRQKQKWERKIIIGFSGHQMVDNMGSPQDENVAVR 360
 DB 301 TYDLLYQCCDAQPGASGVYVVRMKRQKQKWERKIIIGFSGHQMVDNMGSPQDENVAVR 360
 QY 361 ITELKVAQICWIKGNVLDREG 383
 DB 361 ITELKVAQICWIKGNVLDREG 383
 RESULT 12
 AAB80258
 ID AAB80258 standard; protein; 383 AA.
 AC AAB80258;
 XX
 DT 24-APR-2001 (first entry)
 XX Human PRO307 protein.
 DE
 XX Human; PRO; dermatological; antipsoriatic; cytostatic; antiinflammatory;
 KW antiParkinsonian neurotropic; neuroprotective; vulnerary; cardiant;
 KW antiangiogenic; vasotropic; antiasthmatic; antirheumatic; cancer;
 KW antiarthritic; antifertility; antidiabetic; antiviral; diabetes;
 KW opthalmological; gene therapy; skin disease; gastrointestinal disorder;
 KW ischaemia; inflammation.
 XX
 OS Homo sapiens.
 XX
 PN WO200104311-A1.
 XX
 PD 18-JAN-2001.
 XX
 XX 22-FEB-2000; 2000WO-US004414.
 PF
 XX 07-JUL-1999; 99US-0143048P.
 PR 26-JUL-1999; 99US-0145698P.
 PR 28-JUL-1999; 99US-0146222P.

PR 08-SEP-1999; 99WO-US020594.
 PR 13-SEP-1999; 99WO-US020944.
 PR 15-SEP-1999; 99WO-US021090.
 PR 15-SEP-1999; 99WO-US021547.
 PR 05-OCT-1999; 99WO-US023089.
 PR 29-NOV-1999; 99WO-US028214.
 PR 30-NOV-1999; 99WO-US028313.
 PR 02-DEC-1999; 99WO-US028564.
 PR 02-DEC-1999; 99WO-US028565.
 PR 16-DEC-1999; 99WO-US030095.
 PR 20-DEC-1999; 99WO-US030911.
 PR 20-DEC-1999; 99WO-US030999.
 PR 05-JAN-2000; 2000WO-US000219.
 XX (GETH) GENENTECH INC.
 PA Ashkenazi AJ, Botstein D, Desnoyers L, Eaton DL, Ferrara N;
 XX Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME, Goddard A;
 PI Godowski PJ, Grimaldi CJ, Gurney AL, Hillan KJ, Kljavin IJ;
 PI Mather JP, Pan J, Paoni NF, Roy MA, Stewart TA, Tumas D;
 PI Williams PM, Wood WI;
 XX WPI; 2001-081051/09.
 DR N-PSDB; AAF72419.
 XX
 PT Sixty one nucleic acids encoding PRO polypeptides which are useful in the
 PT treatment of skin diseases (e.g. psoriasis), cancers (e.g. lung squamous
 PT cell carcinoma) and neurodegenerative diseases (e.g. Alzheimer's
 PT disease).
 XX
 PS Claim 1; Fig 96; 393pp; English.
 XX
 CC The present sequence is one of sixty one novel secreted and transmembrane
 CC PRO polypeptides. The PRO polypeptides are useful for treating skin
 CC diseases (e.g. psoriasis), cancers (e.g. lung squamous cell carcinoma),
 CC gastrointestinal disorders (e.g. enterocolitis), neurodegenerative
 CC diseases (e.g. Alzheimer's disease, Parkinson's disease), wound repair,
 CC cardiovascular disorders (e.g. endometrial bleeding angiogenesis,
 CC ischaemias such as coronary ischaemia, atherosclerosis), inflammatory
 CC disorders (e.g. asthma, rheumatoid arthritis, multiple sclerosis),
 CC infertility, AIDS and diabetes and retinal disorders such as retinitis
 CC pigmentosum. The PRO nucleic acids have applications in molecular
 CC biology, including use as hybridization probes, and in chromosome and
 CC gene mapping
 XX
 SQ Sequence 383 AA;
 Query Match 96.8%; Score 2044; DB 4; Length 383;
 Best Local Similarity 98.4%; Pred. No. 1.1e-141;
 Matches 377; Conservative 1; Mismatches 5; Indels 0; Gaps 0;
 QY 1 MAGIPGLLFLFLCAVGVSPYSAPWKPTWPAYRLPVVLPQSTLNLAKEPFGAEAKLE 60
 DB 1 MAGIPGLLFLFLCAVGVSPYSAPWKPTWPAYRLPVVLPQSTLNLAKEPFGAEAKLE 60
 QY 61 VSSSCGPOCHKGTPLPTYPEAKQYLSYETLYANGSRTEQVGIYILSSGDXAXRDSGS 120
 DB 61 VSSSCGPOCHKGTPLPTYPEAKQYLSYETLYANGSRTEQVGIYILSSGDXAXRDSGS 120
 QY 121 SGSRKRQIYGYDSRFSIFGKDFLLNYPSTSVKLSGTCTGLVAEXHVLTAACHIDG 180
 DB 121 SGSRKRQIYGYDSRFSIFGKDFLLNYPSTSVKLSGTCTGLVAEXHVLTAACHIDG 180
 QY 181 KTYVKGQKLRVGLFKPKFQDGGGRANDSTSAMPEQMKFQWIRKTHVPKGIKGNAND 240
 DB 181 KTYVKGQKLRVGLFKPKFQDGGGRANDSTSAMPEQMKFQWIRKTHVPKGIKGNAND 240
 QY 241 IGMVDYALLELKKPHKPKMKIGVSPPAKQIPGRIHFSGYDNDPQNLVYRFDVKDE 300
 DB 241 IGMVDYALLELKKPHKPKMKIGVSPPAKQIPGRIHFSGYDNDPQNLVYRFDVKDE 300
 QY 301 TYDLLYQCCDAQPGASGVYVVRMKRQKQKWERKIIIGFSGHQMVDNMGSPQDENVAVR 360
 DB 301 TYDLLYQCCDAQPGASGVYVVRMKRQKQKWERKIIIGFSGHQMVDNMGSPQDENVAVR 360

Db	301	TYDLLYQQCDAQSGSGVYVVMKRWKQQQKWERKIIGIFSGHQWVDMNGSPQDFNVAVR	360
Qy	361	ITPLKYAICYWIKGNLYDCREG 383	
Db	361	ITPLKYAICYWIKGNLYDCREG 383	
RESULT 13			
AA48974			
ID	AA48974	standard; protein; 383 AA.	
XX	AA48974;		
XX			
DT	27-MAR-2001	(first entry)	
XX			
DE	Human Zsig13 variant #3, SEQ ID NO:18.		
XX			
KW	Human Zsig13; serine protease; chromosome 11q22.1; elastase homologue;		
KW	glutamyl endopeptidase homologue; factor X homologue; trypsin homologue;		
KW	trypsinogen homologue; mast cell protease homologue;		
KW	collagenase homologue; protein degradation; food processing; brewing;		
KW	alcohol production; laundry detergent component.		
XX			
OS	Homo sapiens.		
XX			
PN	US6153420-A.		
XX			
PD	28-NOV-2000.		
XX			
PF	04-MAY-1998;	98US-00072384.	
XX			
PR	24-APR-1997;	97US-0044185P.	
PR	17-APR-1998;	98US-00062142.	
XX			
PA	(ZYMO) ZYMOGENETICS INC.		
XX			
PI	Sheppard PO;		
XX			
DR	WPI; 2001-060090/07.		
DR	N-PSDB; AAC91784.		
XX			
PT	New isolated serine protease (designated Zsig13), useful in industrial		
PT	processes to degrade unwanted proteins or alter the characteristics of		
PT	protein-containing composition, as well as in industrial applications		
PT	(e.g. brewing).		
XX			
PS	Claim 1; Col 41-44; 26pp; English.		
XX			
CC	The invention relates to human Zsig13 proteins (AAB48972-848974), and to		
CC	DNA encoding them (AAC91782-C91784). The invention also relates to		
CC	expression vectors and host cells comprising a human Zsig13 DNA, and the		
CC	recombinant production of a human Zsig13 protein or its precursor. Zsig13		
CC	is a serine protease, and has significant homology to Bacillus		
CC	licheniformis glutamyl endopeptidase, human clotting factor X, human		
CC	elastase, rat mast cell protease, Streptomyces griseus trypsin, bovine		
CC	trypsinogen, and Hypoderma lineatum collagenase. The gene encoding human		
CC	Zsig13 is located on chromosome 11q22.1. Zsig13 is useful in industrial		
CC	processes to degrade unwanted proteins or alter the characteristics of		
CC	protein-containing compositions. It may also be used in industrial		
CC	applications in which proteases are utilised, including food processing,		
CC	brewing and alcohol production, and as a component of a laundry		
CC	detergent. The present sequence represents a human Zsig13 variant		
XX			
SQ	Sequence 383 AA;		
Query Match			
Best Local Similarity 96.8%; Score 2044; DB 4; Length 383;			
Matches 377; Conservative 1; Mismatches 5; Indels 0; Gaps 0;			
Qy	1	MAGIPGLLFLFLLCAGVGQSPYAPWKTWPAYRLPVVLPQSTLNIAKPDFGAZAKLE	60
Db	1	MAGIPGLLFLFLLCAGVGQSPYAPWKTWPAYRLPVVLPQSTLNIAKPDFGAZAKLE	60

Qy	61	VSSCGPQCHKTPTPTYPEAKQYLSYETLYANGSRTEYQVCIYILSSSGDGAXXRDSGS	120
Db	61	VSSCGPQCHKTPTPTYPEAKQYLSYETLYANGSRTEYQVCIYILSSSGDGAXXRDSGS	120
Qy	121	SGKSRKRQIYGYDSRFSIFGKDFLLNYPFSTSVKLSGTCTGLVAEXHVLTAACHIDG	180
Db	121	SGKSRKRQIYGYDSRFSIFGKDFLLNYPFSTSVKLSGTCTGLVAEXHVLTAACHIDG	180
Qy	181	KTYVKGTKLVRGFLKPKFKDGGRGANDSTAMPQMKFQWIRVKRTHVPKGIKGNAND	240
Db	181	KTYVKGTKLVRGFLKPKFKDGGRGANDSTAMPQMKFQWIRVKRTHVPKGIKGNAND	240
Qy	241	IGMDYDYALLELKPHKPKFKMIGVSPPAKQIPLGGRIHPSGYDNDPBGHLYVRFCDVKDE	300
Db	241	IGMDYDYALLELKPHKPKFKMIGVSPPAKQIPLGGRIHPSGYDNDPBGHLYVRFCDVKDE	300
Qy	301	TYDLLYQQCDAQSGSGVYVVMKRWKQQQKWERKIIGIFSGHQWVDMNGSPQDFNVAVR	360
Db	301	TYDLLYQQCDAQSGSGVYVVMKRWKQQQKWERKIIGIFSGHQWVDMNGSPQDFNVAVR	360
Qy	361	ITPLKYAICYWIKGNLYDCREG 383	
Db	361	ITPLKYAICYWIKGNLYDCREG 383	
RESULT 14			
AAU29048			
ID	AAU29048	standard; protein; 383 AA.	
XX			
AC	AAU29048;		
XX			
DT	18-DEC-2001	(first entry)	
XX			
DE	Human PRO polypeptide sequence #25.		
XX			
KW	PRO polypeptide; mammal; tumour; cancer; human; cattle; horse; sheep;		
KW	dog; cat; pig; goat; rabbit; tumour necrosis factor alpha; TNF-alpha;		
KW	blood; chondrocyte cell; cell proliferation; cell differentiation; colon;		
KW	adrenal; lung; breast; prostate; rectum; cervix; liver; genetic disorder.		
XX			
OS	Homo sapiens.		
XX			
PN	WO200168848-A2.		
XX			
PD	20-SEP-2001.		
XX			
PF	28-FEB-2001; 2001WO-US006520.		
XX			
PR	01-MAR-2000; 2000WO-US005601.		
PR	02-MAR-2000; 2000WO-US005841.		
PR	03-MAR-2000; 2000US-0187202P.		
PR	06-MAR-2000; 2000US-0186968P.		
PR	14-MAR-2000; 2000US-0189320P.		
PR	14-MAR-2000; 2000US-0189328P.		
PR	15-MAR-2000; 2000WO-US006884.		
PR	21-MAR-2000; 2000US-0190828P.		
PR	21-MAR-2000; 2000US-0191007P.		
PR	21-MAR-2000; 2000US-0191048P.		
PR	21-MAR-2000; 2000US-0191314P.		
PR	28-MAR-2000; 2000US-0192655P.		
PR	29-MAR-2000; 2000US-0193032P.		
PR	29-MAR-2000; 2000US-0193053P.		
PR	30-MAR-2000; 2000WO-US008439.		
PR	04-APR-2000; 2000US-0194449P.		
PR	04-APR-2000; 2000US-0194647P.		
PR	11-APR-2000; 2000US-0195975P.		
PR	11-APR-2000; 2000US-0196000P.		
PR	11-APR-2000; 2000US-0196187P.		
PR	11-APR-2000; 2000US-0196690P.		
PR	18-APR-2000; 2000US-0196820P.		
PR	18-APR-2000; 2000US-0198121P.		
PR	25-APR-2000; 2000US-0199397P.		


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Qy 61 VSSSCGQCHKGTPLPTYKEAKOYLSYETLYANGSRTEXQVGIYILSSSGDGAXXRDSGS 120
Db 61 VSSSCGQCHKGTPLPTYKEAKOYLSYETLYANGSRTEXQVGIYILSSSGDGAXXRDSGS 120

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Db 121 SGKSRKRQIYGYDSRFSIFGKDFLLNYPFSTSVKLGCTGTTLVAEXHVLTAACHIDG 180

Qy 181 KTVYKGTQKLRVGLKPKFKDGGGRGANDSTSAMPEQMKFQWIRVKRTHVPKGIKGNAND 240
Db 181 KTVYKGTQKLRVGLKPKFKDGGGRGANDSTSAMPEQMKFQWIRVKRTHVPKGIKGNAND 240

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Db 241 IGMDYDVALLELKKPKRKFPMKIGVSPPAKQLPGGRHFSGYDNDRPGNLVYRFCVXDE 300

Qy 301 TYDLLYQCCDAQPGASGYVYVWMKQKQKWERKIIGIFSGHGWDMNGSPQDFNVAVR 360
Db 301 TYDLLYQCCDAQPGASGYVYVWMKQKQKWERKIIGIFSGHGWDMNGSPQDFNVAVR 360

Qy 361 ITPKYAQICYWIKGNVLDREG 383
Db 361 ITPKYAQICYWIKGNVLDREG 383

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Search completed: July 1, 2005, 21:03:26
Job time : 104.435 secs

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OM protein - protein search, using sw model

Run on: July 1, 2005, 20:57:14 ; Search time 26.5364 Seconds
(without alignments)
1102.727 Million cell updates/sec

Title: US-09-658-677-2

Perfect score: 2112

Sequence: 1 MAGIPGLFLLFLLCAVGQ.....IKGNVLDRCRGDTVFLPGSN 392

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2104	99.6	392	3	US-09-072-384-2
2	2085	98.7	392	3	Sequence 2, Appl
3	2044	96.8	383	3	Sequence 15, Appl
4	2044	96.8	383	4	Sequence 18, Appl
5	2044	96.8	383	4	Sequence 261, App
6	2044	96.8	383	4	Sequence 261, App
7	2044	96.8	383	4	Sequence 261, App
8	2044	96.8	383	4	Sequence 261, App
9	2044	96.8	383	4	Sequence 261, App
10	2044	96.8	383	4	Sequence 261, App
11	2044	96.8	383	4	Sequence 261, App
12	2044	96.8	383	4	Sequence 261, App
13	190.5	9.0	314	4	Sequence 6, Appl
14	184	8.7	316	4	Sequence 2, Appl
15	166	7.9	318	4	Sequence 10, Appl
16	165	7.8	222	1	Sequence 1, Appl
17	165	7.8	222	2	Sequence 1, Appl
18	165	7.8	222	4	Sequence 1, Appl
19	133.5	6.3	239	4	Sequence 3471, Ap
20	132	6.2	433	4	Sequence 8220, Ap
21	130.5	6.2	313	4	Sequence 14, Appl
22	125	5.9	218	4	Sequence 3950, Ap
23	123	5.8	256	3	Sequence 89, Appl
24	123	5.8	256	3	Sequence 89, Appl
25	123	5.8	256	3	Sequence 89, Appl
26	123	5.8	256	3	Sequence 89, Appl
27	123	5.8	256	3	Sequence 89, Appl

28 123 5.8 256 3 US-09-032-215-32 Sequence 32, Appl
29 123 5.8 256 3 US-09-012-692-89 Sequence 89, Appl
30 123 5.8 256 3 US-08-906-613-89 Sequence 89, Appl
31 123 5.8 256 5 PCT-US95-14442A-89 Sequence 89, Appl
32 122 5.8 320 4 US-09-489-039A-13989 Sequence 13989, A
33 121.5 5.8 238 4 US-09-664-595A-15 Sequence 15, Appl
34 121.5 5.8 302 4 US-09-551-826D-12 Sequence 12, Appl
35 121.5 5.8 437 1 US-08-487-037-2 Sequence 2, Appl
36 120 5.7 303 4 US-09-551-826D-8 Sequence 8, Appl
37 118 5.6 241 3 US-08-944-483-59 Sequence 59, Appl
38 117 5.5 356 4 US-09-902-540-12881 Sequence 12881, A
39 116.5 5.5 437 1 US-08-487-037-3 Sequence 3, Appl
40 116 5.5 488 4 US-09-367-777-44 Sequence 44, Appl
41 116 5.5 488 4 US-09-367-791A-27 Sequence 27, Appl
42 115.5 5.5 691 4 US-09-949-016-7775 Sequence 7775, Ap
43 114 5.4 254 1 US-08-330-978-3 Sequence 3, Appl
44 114 5.4 254 1 US-08-474-042-3 Sequence 3, Appl
45 114 5.4 254 1 US-08-484-558-3 Sequence 3, Appl

ALIGNMENTS

RESULT 1
US-09-072-384-2
; Sequence 2, Application US/09072384
; Patent No. 6153420
; GENERAL INFORMATION:
; APPLICANT: Sheppard, Paul O.
; TITLE OF INVENTION: SERINE PROTEASE POLYPEPTIDES
; TITLE OF INVENTION: AND MATERIALS AND METHODS FOR MAKING THEM
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ZymoGenetics, Inc.
; STREET: 1201 Eastlake Avenue East
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98102
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/072,384
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Parker, Gary E
; REGISTRATION NUMBER: 31,648
; REFERENCE/DOCKET NUMBER: 97-16C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-442-6673
; TELEFAX: 206-442-6678
; TELEX:
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 392 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
; FEATURE:
; NAME/KEY: Signal Sequence
; LOCATION: 1...19
; OTHER INFORMATION:
; US-09-072-384-2

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Best Local Similarity 100.0%; Pred. No. 5.2e-218;
Matches 392; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 MAGIPGLLFLFLLCAVGVSPYSAPWKPPTWPAYRLPVVLPQSTLNLAKEPFGAEAKLE 60
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QY 61 VSSSCGPOCHKGTPPTYKEAKQYLSYETLYANGSRTEXQVGIYILSSSGDGAXXRDSGS 120
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QY 181 KTVVKGTKLRVGLFKPKFKDGGRGANDSTSAMPEQMKFQWIRVKTHTVPKGIKNAND 240
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Db 181 KTVVKGTKLRVGLFKPKFKDGGRGANDSTSAMPEQMKFQWIRVKTHTVPKGIKNAND 240
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QY 241 IGMDDYALLENLKKPHKRFKMGKIGVSPPAKQLPGGRIHFSGYDNDPRGNLVYRFCVDKDE 300
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Db 241 IGMDDYALLENLKKPHKRFKMGKIGVSPPAKQLPGGRIHFSGYDNDPRGNLVYRFCVDKDE 300
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QY 301 TYDLLYQCCDAQPGASGYGVYVVMKRWKQKWKRIIGIFSGHWDMMNGSPQDFNVAVR 360
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QY 361 ITPLKYAQICYWIKGNLYDCREGDTVFLPGSN 392
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RESULT 2
US-09-072-384-15
; Sequence 15, Application US/09072384
; Patent No. 6153420
; GENERAL INFORMATION:
; APPLICANT: Sheppard, Paul O.
; TITLE OF INVENTION: SERINE PROTEASE POLYPEPTIDES
; TITLE OF INVENTION: AND MATERIALS AND METHODS FOR MAKING THEM
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ZymoGenetics, Inc.
; STREET: 1201 Eastlake Avenue East
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98102
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/072,384
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Parker, Gary E
; REGISTRATION NUMBER: 31,648
; REFERENCE/DOCKET NUMBER: 97-16C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-442-6673
; TELEFAX: 206-442-6678
; TELEX:
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 392 amino acids
; TYPE: amino acid
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STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
FRAGMENT TYPE: internal
FEATURE:
NAME/KEY: Signal Sequence
LOCATION: 1...19
OTHER INFORMATION:
US-09-072-384-15

Query Match      98.7%; Score 2085; DB 3; Length 392;
Best Local Similarity 98.2%; Pred. No. 5.9e-216;
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    |||
Db 61 VSSSCGPOCHKGTPPTYKEAKQYLSYETLYANGSRTEXQVGIYILSSSGDGAXXRDSGS 120
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QY 121 SGKSRKRQIYGYDSRFSIFGKDFLLNYPFSTSVKLTGCTGTLVAEXHVLTAACHIDG 180
    |||
Db 121 SGKSRKRQIYGYDSRFSIFGKDFLLNYPFSTSVKLTGCTGTLVAEXHVLTAACHIDG 180
    |||

QY 181 KTVVKGTKLRVGLFKPKFKDGGRGANDSTSAMPEQMKFQWIRVKTHTVPKGIKNAND 240
    |||
Db 181 KTVVKGTKLRVGLFKPKFKDGGRGANDSTSAMPEQMKFQWIRVKTHTVPKGIKNAND 240
    |||

QY 241 IGMDDYALLENLKKPHKRFKMGKIGVSPPAKQLPGGRIHFSGYDNDPRGNLVYRFCVDKDE 300
    |||
Db 241 IGMDDYALLENLKKPHKRFKMGKIGVSPPAKQLPGGRIHFSGYDNDPRGNLVYRFCVDKDE 300
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QY 301 TYDLLYQCCDAQPGASGYGVYVVMKRWKQKWKRIIGIFSGHWDMMNGSPQDFNVAVR 360
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Db 301 TYDLLYQCCDAQPGASGYGVYVVMKRWKQKWKRIIGIFSGHWDMMNGSPQDFNVAVR 360
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QY 361 ITPLKYAQICYWIKGNLYDCREGDTVFLPGSN 392
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Db 361 ITPLKYAQICYWIKGNLYDCREGDTVFLPGSN 392
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RESULT 3
US-09-072-384-18
; Sequence 18, Application US/09072384
; Patent No. 6153420
; GENERAL INFORMATION:
; APPLICANT: Sheppard, Paul O.
; TITLE OF INVENTION: SERINE PROTEASE POLYPEPTIDES
; TITLE OF INVENTION: AND MATERIALS AND METHODS FOR MAKING THEM
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ZymoGenetics, Inc.
; STREET: 1201 Eastlake Avenue East
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98102
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/072,384
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Parker, Gary E
```


REGISTRATION NUMBER: 31,648
REFERENCE/DOCKET NUMBER: 97-16C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-442-6673
TELEFAX: 206-442-6678
TELEX:

INFORMATION FOR SEQ ID NO: 18:

SEQUENCE CHARACTERISTICS:

LENGTH: 383 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: protein

FRAGMENT TYPE: internal

FEATURE:

NAME/KEY: Signal Sequence

LOCATION: 1...19

OTHER INFORMATION:

US-09-072-384-18

Query Match 96.8%; Score 2044; DB 3; Length 383;
Best Local Similarity 98.4%; Pred. No. 1.5e-211;
Matches 377; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

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DB 1 MAGIPGLLFLFLLCVAVGVSPYSAPWKPWPAYRLPVVLPSTLNLAKPDFGAEAKLE 60

QY 61 VSSSCGPOCHKGTPLTYEAKQYLSYETLYANGSRTEQVGIYILSSSGDGAXXRDSGS 120
DB 61 VSSSCGPOCHKGTPLTYEAKQYLSYETLYANGSRTEQVGIYILSSSGDGAXXRDSGS 120

QY 121 SGKSRKRQIYGYDSRFSIFGKDFLLNYPFSTSVKLSGTCTGLTVAEXHVLTAACHIDG 180
DB 121 SGKSRKRQIYGYDSRFSIFGKDFLLNYPFSTSVKLSGTCTGLTVAEXHVLTAACHIDG 180

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DB 181 KTYVKGTKLRVGLFKPKFDGGRGANDSTSAMPEQMKFQWIRVKTTHVPKGIKGNAND 240

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QY 301 TYDLLVQCCDAQPGASGYVYRWKQKQKWERKIIGIFSGHWDVMDNGSPQDFNVAVR 360
DB 301 TYDLLVQCCDAQPGASGYVYRWKQKQKWERKIIGIFSGHWDVMDNGSPQDFNVAVR 360

QY 361 ITPLKVAQICWIKGNVLDREG 383
DB 361 ITPLKVAQICWIKGNVLDREG 383

RESULT 4

US-09-907-794A-261
Sequence 261, Application US/09907794A

Patent No. 6635468

GENERAL INFORMATION:

APPLICANT: Genentech, Inc.

APPLICANT: Ashkenazi, Avi

APPLICANT: Botstein, David

APPLICANT: Desnovers, Luc

APPLICANT: Eaton, Dan L.

APPLICANT: Ferrara, Napoleone

APPLICANT: Filvaroff, Ellen

APPLICANT: Fong, Sherman

APPLICANT: Gao, Wei-Qiang

APPLICANT: Gerber, Hanspeter

APPLICANT: Griggs, Mary E.

APPLICANT: Goddard, A.

APPLICANT: Godowski, Paul J.

APPLICANT: Grimaldi, Christopher J.

APPLICANT: Gurney, Austin L.

APPLICANT:

APPLICANT: Hillan, Kenneth, J.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Mather, Jennie P.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: 10466-14
CURRENT APPLICATION NUMBER: US/09/907,794A
CURRENT FILING DATE: 2001-07-17
PRIOR APPLICATION NUMBER: PCT/US00/04414
PRIOR FILING DATE: 2000-02-22
PRIOR APPLICATION NUMBER: US 60/143,048
PRIOR FILING DATE: 1999-07-07
PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR FILING DATE: 1999-07-26
PRIOR APPLICATION NUMBER: US 60/146,222
PRIOR FILING DATE: 1999-07-28
PRIOR APPLICATION NUMBER: PCT/US99/20594
PRIOR FILING DATE: 1999-09-08
PRIOR APPLICATION NUMBER: PCT/US99/20944
PRIOR FILING DATE: 1999-09-13
PRIOR APPLICATION NUMBER: PCT/US99/21090
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/21547
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/23089
PRIOR FILING DATE: 1999-10-05
PRIOR APPLICATION NUMBER: PCT/US99/28214
PRIOR FILING DATE: 1999-11-29
PRIOR APPLICATION NUMBER: PCT/US99/28313
PRIOR FILING DATE: 1999-11-30
PRIOR APPLICATION NUMBER: PCT/US99/28564
PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/28565
PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/30095
PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: PCT/US99/30911
PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US99/30999
PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US00/00219
PRIOR FILING DATE: 2000-01-05
NUMBER OF SEQ ID NOS: 423
SEQ ID NO 261
LENGTH: 383
TYPE: PRT
ORGANISM: Homo Sapien
US-09-907-794A-261

Query Match 96.8%; Score 2044; DB 4; Length 383;
Best Local Similarity 98.4%; Pred. No. 1.5e-211;
Matches 377; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 1 MAGIPGLLFLFLLCVAVGVSPYSAPWKPWPAYRLPVVLPSTLNLAKPDFGAEAKLE 60
DB 1 MAGIPGLLFLFLLCVAVGVSPYSAPWKPWPAYRLPVVLPSTLNLAKPDFGAEAKLE 60

QY 61 VSSSCGPOCHKGTPLTYEAKQYLSYETLYANGSRTEQVGIYILSSSGDGAXXRDSGS 120
DB 61 VSSSCGPOCHKGTPLTYEAKQYLSYETLYANGSRTEQVGIYILSSSGDGAXXRDSGS 120

QY 121 SGKSRKRQIYGYDSRFSIFGKDFLLNYPFSTSVKLSGTCTGLTVAEXHVLTAACHIDG 180
DB 121 SGKSRKRQIYGYDSRFSIFGKDFLLNYPFSTSVKLSGTCTGLTVAEXHVLTAACHIDG 180

QY 181 KTYVKGTKLRVGLFKPKFDGGRGANDSTSAMPEQMKFQWIRVKTTHVPKGIKGNAND 240

Db 181 KTVVGTQKLRVGLPKFKDGGGANDSTSAPEQKQFQWIRVXKTHVPGWIKGNAND 240
Qy 241 IGMDYDVALLELKKPKRKFMIKGVSPPAKQLPGGRIFHSGYDNDPRGNLVYRFCVDKDE 300
Db 241 IGMDYDVALLELKKPKRKFMIKGVSPPAKQLPGGRIFHSGYDNDPRGNLVYRFCVDKDE 300
Qy 301 TYDLLYQQCDAQPGASGVYVYRMWKRQOQKWERKIIIGIFSGHWDVMDNGSPQDFNVAVR 360
Db 301 TYDLLYQQCDAQPGASGVYVYRMWKRQOQKWERKIIIGIFSGHWDVMDNGSPQDFNVAVR 360
Qy 361 ITPLKYAQICYWIKGNLYDCREG 383
Db 361 ITPLKYAQICYWIKGNLYDCREG 383

RESULT 5
US-09-905-125A-261
; Sequence 261, Application US/09905125A
; Patent No. 6664376
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/905,125A
; PRIOR FILING DATE: 2001-07-12
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30

; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 261
; LENGTH: 383
; TYPE: PRT
; ORGANISM: Homo Sapien
US-09-905-125A-261
Query Match 96.8%; Score 2044; DB 4; Length 383;
Best Local Similarity 98.4%; Pred. No. 1.5e-211;
Matches 377; Conservative 1; Mismatches 5; Indels 0; Gaps 0;
Qy 1 MAGIPGLLELLEFLICAVQVSPYSAPWKPWPAYRLPVVLPQSTLNIAKPDGAEAKLE 60
Db 1 MAGIPGLLELLEFLICAVQVSPYSAPWKPWPAYRLPVVLPQSTLNIAKPDGAEAKLE 60
Qy 61 VSSSCGPOCHKGTPLPTYKEAKQYLSYETLYANGSRTEXQVGIYILSSSGDGAXXRDSGS 120
Db 61 VSSSCGPOCHKGTPLPTYEEAKQYLSYETLYANGSRTEQVGIYILSSSGDGQAHRDSGS 120
Qy 121 SGKSRKRQIYGYDSRFSIFGKDFLLNYPFSTS VKLSTGCTGTLVAEXHVLTAACHIDG 180
Db 121 SGKSRKRQIYGYDSRFSIFGKDFLLNYPFSTS VKLSTGCTGTLVAEXHVLTAACHIDG 180
Qy 181 KTYVGTQKLRVGLPKFKDGGGANDSTSAPEQKQFQWIRVXKTHVPGWIKGNAND 240
Db 181 KTYVGTQKLRVGLPKFKDGGGANDSTSAPEQKQFQWIRVXKTHVPGWIKGNAND 240
Qy 241 IGMDYDVALLELKKPKRKFMIKGVSPPAKQLPGGRIFHSGYDNDPRGNLVYRFCVDKDE 300
Db 241 IGMDYDVALLELKKPKRKFMIKGVSPPAKQLPGGRIFHSGYDNDPRGNLVYRFCVDKDE 300
Qy 301 TYDLLYQQCDAQPGASGVYVYRMWKRQOQKWERKIIIGIFSGHWDVMDNGSPQDFNVAVR 360
Db 301 TYDLLYQQCDAQPGASGVYVYRMWKRQOQKWERKIIIGIFSGHWDVMDNGSPQDFNVAVR 360
Qy 361 ITPLKYAQICYWIKGNLYDCREG 383
Db 361 ITPLKYAQICYWIKGNLYDCREG 383
RESULT 6
US-09-902-775A-261
; Sequence 261, Application US/09902775A
; Patent No. 6686451
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.

APPLICANT: Kijavin, Ivar J.
APPLICANT: Mather, Jennie P.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: 10466-14
CURRENT FILING DATE: 2001-07-10
CURRENT APPLICATION NUMBER: US/09/902.775A
PRIOR FILING DATE: 2000-02-22
PRIOR APPLICATION NUMBER: PCT/US00/04414
PRIOR FILING DATE: 2000-02-22
PRIOR APPLICATION NUMBER: US 60/143,048
PRIOR FILING DATE: 1999-07-07
PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR FILING DATE: 1999-07-26
PRIOR APPLICATION NUMBER: US 60/146,222
PRIOR FILING DATE: 1999-07-28
PRIOR APPLICATION NUMBER: PCT/US99/20594
PRIOR FILING DATE: 1999-09-08
PRIOR APPLICATION NUMBER: PCT/US99/20594
PRIOR FILING DATE: 1999-09-08
PRIOR APPLICATION NUMBER: PCT/US99/20944
PRIOR FILING DATE: 1999-09-13
PRIOR APPLICATION NUMBER: PCT/US99/21090
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/21547
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/23089
PRIOR FILING DATE: 1999-10-05
PRIOR APPLICATION NUMBER: PCT/US99/28214
PRIOR FILING DATE: 1999-11-29
PRIOR APPLICATION NUMBER: PCT/US99/28313
PRIOR FILING DATE: 1999-11-30
PRIOR APPLICATION NUMBER: PCT/US99/28564

Query Match 96.8%; Score 2044; DB 4; Length 383;
Best Local Similarity 98.4%; Pred. No. 1.5e-211;
Matches 377; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 1 MAGIPGLLFLFLLCAGGVSPYSAPWKPMPAYRLPVVLPSTLNLAKEPFGAEAKLE 60
DB 1 MAGIPGLLFLFLLCAGGVSPYSAPWKPMPAYRLPVVLPSTLNLAKEPFGAEAKLE 60
QY 61 VSSSCGPOCHKGTPLPTYEAKQVLSYETLYANGSRTEKQVGYIYSSSGDGAXXRDSGS 120
DB 61 VSSSCGPOCHKGTPLPTYEAKQVLSYETLYANGSRTEKQVGYIYSSSGDGAXXRDSGS 120
QY 121 SGKSRKRQIYGYDSRFSIFGKDFLLNYPFSTSVKLSGTGTLVAEXHVLTAACHIDG 180
DB 121 SGKSRKRQIYGYDSRFSIFGKDFLLNYPFSTSVKLSGTGTLVAEXHVLTAACHIDG 180
QY 181 KTYVGTQKLRVGLKPKFKDGGGRANDSTSAMPEQMKFQWIRVKTTHVPKGIKNAND 240

DB 181 KTYVGTQKLRVGLKPKFKDGGGRANDSTSAMPEQMKFQWIRVKTTHVPKGIKNAND 240
QY 241 IGMDDYALLELEKPKHKKEMKIGVSPPAKOLPGRIFHSGYDNDRCNLVYRCDVKDE 300
DB 241 IGMDDYALLELEKPKHKKEMKIGVSPPAKOLPGRIFHSGYDNDRCNLVYRCDVKDE 300
QY 301 TYDLLYQOCDAPGASGYGVYVVMWKRQOQKWKRIIGIFSGHWDVMDNGSPQDFNVAVR 360
DB 301 TYDLLYQOCDAPGASGYGVYVVMWKRQOQKWKRIIGIFSGHWDVMDNGSPQDFNVAVR 360
QY 361 ITELKVAQICYMIKGNLYDCREG 383
DB 361 ITELKVAQICYMIKGNLYDCREG 383

RESULT 7
US-09-906-700-261
Sequence 261, Application US/09906700
Patent No. 6723535
GENERAL INFORMATION:
APPLICANT: Genentech, Inc.
APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, A.
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, Christopher J.
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth, J.
APPLICANT: Kijavin, Ivar J.
APPLICANT: Mather, Jennie P.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: 10466-14
CURRENT APPLICATION NUMBER: US/09/906,700
CURRENT FILING DATE: 2000-09-18
PRIOR APPLICATION NUMBER: PCT/US00/04414
PRIOR FILING DATE: 2000-02-22
PRIOR APPLICATION NUMBER: US 60/143,048
PRIOR FILING DATE: 1999-07-07
PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR FILING DATE: 1999-07-26
PRIOR APPLICATION NUMBER: US 60/146,222
PRIOR FILING DATE: 1999-07-28
PRIOR APPLICATION NUMBER: PCT/US99/20594
PRIOR FILING DATE: 1999-09-08
PRIOR APPLICATION NUMBER: PCT/US99/20944
PRIOR FILING DATE: 1999-09-13
PRIOR APPLICATION NUMBER: PCT/US99/21090
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/21547
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/23089
PRIOR FILING DATE: 1999-10-05
PRIOR APPLICATION NUMBER: PCT/US99/28214
PRIOR FILING DATE: 1999-11-29
PRIOR APPLICATION NUMBER: PCT/US99/28313
PRIOR FILING DATE: 1999-11-30
PRIOR APPLICATION NUMBER: PCT/US99/28564

; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 261
; LENGTH: 383
; TYPE: PRT
; ORGANISM: Homo Sapien
US-09-906-700-261

Query Match
Best Local Similarity 96.8%; Score 2044; DB 4; Length 383;
Matches 377; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 1 MAGIPGLLFLFLLCAGGVSPYSAPWKPPTWPAVRLPVVLPQSTLNLAKEPFGAEAKLE 60
DB 1 MAGIPGLLFLFLLCAGGVSPYSAPWKPPTWPAVRLPVVLPQSTLNLAKEPFGAEAKLE 60

QY 61 VSSSCGPGQCHKGTPLPTTYEAKQYLSYETLYANGSRTEXQVGIYIILSSSGDGAXXRDSGS 120
DB 61 VSSSCGPGQCHKGTPLPTTYEAKQYLSYETLYANGSRTEXQVGIYIILSSSGDGAXXRDSGS 120

QY 121 SGKSRKRQIYGYDSRFSIFGKDFLLNYPFSTSVKLSCTGCTGLVAEXHVLTAHCHIDG 180
DB 121 SGKSRKRQIYGYDSRFSIFGKDFLLNYPFSTSVKLSCTGCTGLVAEXHVLTAHCHIDG 180

QY 181 KTYVKGTKLRVGLFKPKDGGGRANDSTSAMPEQMKFQWIRVKRTHVPKGIKNAND 240
DB 181 KTYVKGTKLRVGLFKPKDGGGRANDSTSAMPEQMKFQWIRVKRTHVPKGIKNAND 240

QY 241 IGMDDYDYLLELKKPKHFKMKGIVSPPAKQLPGRHIFSGYDNDPRGNLVRFCVDKDE 300
DB 241 IGMDDYDYLLELKKPKHFKMKGIVSPPAKQLPGRHIFSGYDNDPRGNLVRFCVDKDE 300

QY 301 TYDLLYQQCDAQPGASGSGYVVMWKRQOQKWERKIIGIFSGHQWDMNGSPQDFNVAVR 360
DB 301 TYDLLYQQCDAQPGASGSGYVVMWKRQOQKWERKIIGIFSGHQWDMNGSPQDFNVAVR 360

QY 361 ITPKYAQICYWKGNLYDCREG 383
DB 361 ITPKYAQICYWKGNLYDCREG 383

RESULT 8
US-09-903-603A-261
; Sequence 261, Application US/09903603A
; Patent No. 6767995
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.

; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: GNE.1618P2C12
; CURRENT APPLICATION NUMBER: US/09/903,603A
; CURRENT FILING DATE: 2001-07-11
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 261
; LENGTH: 383
; TYPE: PRT
; ORGANISM: Homo Sapien
US-09-903-603A-261

Query Match
Best Local Similarity 96.8%; Score 2044; DB 4; Length 383;
Matches 377; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 1 MAGIPGLLFLFLLCAGGVSPYSAPWKPPTWPAVRLPVVLPQSTLNLAKEPFGAEAKLE 60
DB 1 MAGIPGLLFLFLLCAGGVSPYSAPWKPPTWPAVRLPVVLPQSTLNLAKEPFGAEAKLE 60

QY 61 VSSSCGPGQCHKGTPLPTTYEAKQYLSYETLYANGSRTEXQVGIYIILSSSGDGAXXRDSGS 120
DB 61 VSSSCGPGQCHKGTPLPTTYEAKQYLSYETLYANGSRTEXQVGIYIILSSSGDGAXXRDSGS 120

QY 121 SGKSRKRQIYGYDSRFSIFGKDFLLNYPFSTSVKLSCTGCTGLVAEXHVLTAHCHIDG 180
DB 121 SGKSRKRQIYGYDSRFSIFGKDFLLNYPFSTSVKLSCTGCTGLVAEXHVLTAHCHIDG 180

QY 181 KTYVKGTKLRVGLFKPKDGGGRANDSTSAMPEQMKFQWIRVKRTHVPKGIKNAND 240
DB 181 KTYVKGTKLRVGLFKPKDGGGRANDSTSAMPEQMKFQWIRVKRTHVPKGIKNAND 240

QY 241 IGMDYDVALLELKKPHKFKFKWIGVSPAKQLPGGRHFGSYDNDPRGNLVYRFDVKDE 300
 Db 241 IGMDYDVALLELKKPHKFKFKWIGVSPAKQLPGGRHFGSYDNDPRGNLVYRFDVKDE 300
 QY 301 TYDLYQQCDAOPGASGYVYRWMKQOQKWERKIIGIFSGHQWVDMNGSPQDFNVAVR 360
 Db 301 TYDLYQQCDAOPGASGYVYRWMKQOQKWERKIIGIFSGHQWVDMNGSPQDFNVAVR 360
 QY 361 ITPLKYAQICYWIKGNLYDCREG 383
 Db 361 ITPLKYAQICYWIKGNLYDCREG 383

RESULT 9
 US-09-904-920A-261
 ; Sequence 261, Application US/09904920A
 ; Patent No. 6806352
 ; GENERAL INFORMATION:
 ; APPLICANT: Genentech, Inc.
 ; APPLICANT: Ashkenazi, Avi
 ; APPLICANT: Botstein, David
 ; APPLICANT: Desnoyers, Luc
 ; APPLICANT: Baton, Dan L.
 ; APPLICANT: Ferrara, Napoleone
 ; APPLICANT: Filvaroff, Ellen
 ; APPLICANT: Fong, Sherman
 ; APPLICANT: Gao, Wei-Qiang
 ; APPLICANT: Gerber, Hanspeter
 ; APPLICANT: Gerritsen, Mary E.
 ; APPLICANT: Goddard, A.
 ; APPLICANT: Godowski, Paul J.
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 ; APPLICANT: Hillan, Kenneth, J.
 ; APPLICANT: Kijavlin, Ivar J.
 ; APPLICANT: Mather, Jennie P.
 ; APPLICANT: Pan, James
 ; APPLICANT: Paoni, Nicholas F.
 ; APPLICANT: Roy, Margaret Ann
 ; APPLICANT: Stewart, Timothy A.
 ; APPLICANT: Tumas, Daniel
 ; APPLICANT: Williams, P. Mickey
 ; APPLICANT: Wood, William, I.
 ; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
 ; FILE OF INVENTION: Acids Encoding the Same
 ; FILE REFERENCE: 10466-14
 ; CURRENT APPLICATION NUMBER: US/09/904,920A
 ; CURRENT FILING DATE: 2001-07-13
 ; PRIOR APPLICATION NUMBER: PCT/US00/04414
 ; PRIOR FILING DATE: 2000-02-22
 ; PRIOR APPLICATION NUMBER: US 60/143,048
 ; PRIOR FILING DATE: 1999-07-07
 ; PRIOR APPLICATION NUMBER: US 60/145,698
 ; PRIOR FILING DATE: 1999-07-26
 ; PRIOR APPLICATION NUMBER: US 60/146,222
 ; PRIOR FILING DATE: 1999-07-28
 ; PRIOR APPLICATION NUMBER: PCT/US99/20594
 ; PRIOR FILING DATE: 1999-09-08
 ; PRIOR APPLICATION NUMBER: PCT/US99/20944
 ; PRIOR FILING DATE: 1999-09-13
 ; PRIOR APPLICATION NUMBER: PCT/US99/21090
 ; PRIOR FILING DATE: 1999-09-15
 ; PRIOR APPLICATION NUMBER: PCT/US99/21547
 ; PRIOR FILING DATE: 1999-09-15
 ; PRIOR APPLICATION NUMBER: PCT/US99/23089
 ; PRIOR FILING DATE: 1999-10-05
 ; PRIOR APPLICATION NUMBER: PCT/US99/28214
 ; PRIOR FILING DATE: 1999-11-29
 ; PRIOR APPLICATION NUMBER: PCT/US99/28313
 ; PRIOR FILING DATE: 1999-11-30
 ; PRIOR APPLICATION NUMBER: PCT/US99/28564
 ; PRIOR FILING DATE: 1999-12-02

; PRIOR APPLICATION NUMBER: PCT/US99/28565
 ; PRIOR FILING DATE: 1999-12-02
 ; PRIOR APPLICATION NUMBER: PCT/US99/30095
 ; PRIOR FILING DATE: 1999-12-16
 ; PRIOR APPLICATION NUMBER: PCT/US99/30911
 ; PRIOR FILING DATE: 1999-12-20
 ; PRIOR APPLICATION NUMBER: PCT/US99/30999
 ; PRIOR FILING DATE: 1999-12-20
 ; PRIOR APPLICATION NUMBER: PCT/US00/00219
 ; PRIOR FILING DATE: 2000-01-05
 ; NUMBER OF SEQ ID NOS: 423
 ; SEQ ID NO 261
 ; LENGTH: 383
 ; TYPE: PRT
 ; ORGANISM: Homo Sapien
 ; US-09-904-920A-261
 Query Match 96.8%; Score 2044; DB 4; Length 383;
 Best Local Similarity 98.4%; Pred. No. 1.5e-211;
 Matches 377; Conservative 1; Mismatches 5; Indels 0; Gaps 0;
 QY 1 MAGIPGLLFLFPCLLCAGVQVSPYSAPWKPPTWPAAYRLPVVLPSTLNLAKPDPFGAEAKLE 60
 Db 1 MAGIPGLLFLFPCLLCAGVQVSPYSAPWKPPTWPAAYRLPVVLPSTLNLAKPDPFGAEAKLE 60
 QY 61 VSSSCGPOCHKGTPLTYKEAQYLSYETLYANGSRTEQVGIYIILSSSGDGAXXRDSGS 120
 Db 61 VSSSCGPOCHKGTPLTYBEAKQYLSYETLYANGSRTEQVGIYIILSSSGDGAXXRDSGS 120
 QY 121 SGKRRKROIYGYDSRFSIFGKDFLLNYPFSTSVKLSCTGTGLVAEXHVLTAACHIDG 180
 Db 121 SGKRRKROIYGYDSRFSIFGKDFLLNYPFSTSVKLSCTGTGLVAEXHVLTAACHIDG 180
 QY 181 KTYVKTQKLRVGFLLKPKFGKGGRGANDSTSAMPEQMKFQWIRVKRTHVPKGIKGNAND 240
 Db 181 KTYVKTQKLRVGFLLKPKFGKGGRGANDSTSAMPEQMKFQWIRVKRTHVPKGIKGNAND 240
 QY 241 IGMDYDVALLELKKPHKFKFKWIGVSPAKQLPGGRHFGSYDNDPRGNLVYRFDVKDE 300
 Db 241 IGMDYDVALLELKKPHKFKFKWIGVSPAKQLPGGRHFGSYDNDPRGNLVYRFDVKDE 300
 QY 301 TYDLYQQCDAOPGASGYVYRWMKQOQKWERKIIGIFSGHQWVDMNGSPQDFNVAVR 360
 Db 301 TYDLYQQCDAOPGASGYVYRWMKQOQKWERKIIGIFSGHQWVDMNGSPQDFNVAVR 360
 QY 361 ITPLKYAQICYWIKGNLYDCREG 383
 Db 361 ITPLKYAQICYWIKGNLYDCREG 383

RESULT 10
 US-09-909-064-261
 ; Sequence 261, Application US/09909064
 ; Patent No. 6818449
 ; GENERAL INFORMATION:
 ; APPLICANT: Genentech, Inc.
 ; APPLICANT: Ashkenazi, Avi
 ; APPLICANT: Botstein, David
 ; APPLICANT: Desnoyers, Luc
 ; APPLICANT: Baton, Dan L.
 ; APPLICANT: Ferrara, Napoleone
 ; APPLICANT: Filvaroff, Ellen
 ; APPLICANT: Fong, Sherman
 ; APPLICANT: Gao, Wei-Qiang
 ; APPLICANT: Gerber, Hanspeter
 ; APPLICANT: Gerritsen, Mary E.
 ; APPLICANT: Goddard, A.
 ; APPLICANT: Godowski, Paul J.
 ; APPLICANT: Grimaldi, Christopher J.
 ; APPLICANT: Gurney, Austin L.
 ; APPLICANT: Hillan, Kenneth, J.
 ; APPLICANT: Kijavlin, Ivar J.
 ; APPLICANT: Mather, Jennie P.

```

; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/909,064
; CURRENT FILING DATE: 2001-07-18
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 261
; LENGTH: 383
; TYPE: PRT
; ORGANISM: Homo Sapien
; US-09-909-064-261

Query Match 96.8%; Score 2044; DB 4; Length 383;
Best Local Similarity 98.4%; Pred. No. 1.5e-211;
Matches 377; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

Qy 1 MAGIPGLLFLFLLCAGVGQSPVSPAPKPTWPAYRLPVVLPOSTLNLAKEPFGAEAKLE 60
Db 1 MAGIPGLLFLFLLCAGVGQSPVSPAPKPTWPAYRLPVVLPOSTLNLAKEPFGAEAKLE 60

Qy 61 VSSSCGPGCHKGTPLPYKEAKQYLSYETLLYANGSRTEXQVGYIILSSSGDGAXXRDSGS 120
Db 61 VSSSCGPGCHKGTPLPYKEAKQYLSYETLLYANGSRTEXQVGYIILSSSGDGAXXRDSGS 120

Qy 121 SGSKRRKQIYGYDSRFSIFGKDFLLNYPSTSVKLSGTGTLVAEKHVLTAACHIDHG 180
Db 121 SGSKRRKQIYGYDSRFSIFGKDFLLNYPSTSVKLSGTGTLVAEKHVLTAACHIDHG 180

Qy 181 KTVYKGTQKLRVFLKPKFKDGGGRGANDSTSAMPEQMKFQWIRVKRTHVPKGIKNAND 240
Db 181 KTVYKGTQKLRVFLKPKFKDGGGRGANDSTSAMPEQMKFQWIRVKRTHVPKGIKNAND 240

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Qy 241 IGMDDYDVALLELKPKHKFKPMKIGVSPPAKQIPGGRHFSGYDNDPGLNLYRFCDDVKE 300
Db 241 IGMDDYDVALLELKPKHKFKPMKIGVSPPAKQIPGGRHFSGYDNDPGLNLYRFCDDVKE 300

Qy 301 TYDLYQQCDAOPGASGVGVYVMMKROQKWKRIIGIFSGHQWYDMNGSPQDFNVAVR 360
Db 301 TYDLYQQCDAOPGASGVGVYVMMKROQKWKRIIGIFSGHQWYDMNGSPQDFNVAVR 360

Qy 361 ITPLKYAQICYWIKGNLYLDCREG 383
Db 361 ITPLKYAQICYWIKGNLYLDCREG 383

RESULT 11
US-09-905-381A-261
; Sequence 261, Application US/09905381A
; Patent No. 6818746
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/905,381A
; CURRENT FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
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; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565

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; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 261
; LENGTH: 383
; TYPE: PRT
; ORGANISM: Homo Sapien
US-09-905-381A-261

Query Match          96.8%; Score 2044; DB 4; Length 383;
Best Local Similarity 98.4%; Pred. No. 1.5e-211;
Matches 377; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 1 MAGIPGLLELLFLLCAVGVSPYSAPWKPTWPAYRLPVVLPQSTLNLAKEPFGAEAKLE 60
Db 1 MAGIPGLLELLFLLCAVGVSPYSAPWKPTWPAYRLPVVLPQSTLNLAKEPFGAEAKLE 60
QY 61 VSSSCGPGCHKGTPPTYKEAKQVLSYETLYANGSRTEXQVGIYILSSSGDGAXXRDSGS 120
Db 61 VSSSCGPGCHKGTPPTYKEAKQVLSYETLYANGSRTEXQVGIYILSSSGDGAXXRDSGS 120
QY 121 SGKSRKRQIYGYDSRFSIFGKDFLLNYPFSTSVKLSCTGTLVAEXHVLTAACHIDG 180
Db 121 SGKSRKRQIYGYDSRFSIFGKDFLLNYPFSTSVKLSCTGTLVAEXHVLTAACHIDG 180
QY 181 KTYVKGTKLRVGFLLKPKFKDGGRGANDSTSAMPEQMKFQWIRVKTTHVPKGIKGNAND 240
Db 181 KTYVKGTKLRVGFLLKPKFKDGGRGANDSTSAMPEQMKFQWIRVKTTHVPKGIKGNAND 240
QY 241 IGMVDYVALLLELKKPHKRFKMGKIGVSPAKQLPGGRIFHSGYDNDPRGNLVYRFDVKDE 300
Db 241 IGMVDYVALLLELKKPHKRFKMGKIGVSPAKQLPGGRIFHSGYDNDPRGNLVYRFDVKDE 300
QY 301 TYDLLYQQCDAQPGASGYGVYVRMWRKQOQKWKRIIGIFSGHQWDMNGSPQDFNVAVR 360
Db 301 TYDLLYQQCDAQPGASGYGVYVRMWRKQOQKWKRIIGIFSGHQWDMNGSPQDFNVAVR 360
QY 361 ITPKVAQICYWKGNVLDRCRG 383
Db 361 ITPKVAQICYWKGNVLDRCRG 383

RESULT 12
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; Sequence 261, Application US/09906618
; Patent No. 6828146
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
```

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; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/906,618
; PRIOR FILING DATE: 2001-07-16
; PRIOR APPLICATION NUMBER: PCT/US00/04414
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; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 261
; LENGTH: 383
; TYPE: PRT
; ORGANISM: Homo Sapien
US-09-906-618-261

Query Match          96.8%; Score 2044; DB 4; Length 383;
Best Local Similarity 98.4%; Pred. No. 1.5e-211;
Matches 377; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

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Db 1 MAGIPGLLELLFLLCAVGVSPYSAPWKPTWPAYRLPVVLPQSTLNLAKEPFGAEAKLE 60
QY 61 VSSSCGPGCHKGTPPTYKEAKQVLSYETLYANGSRTEXQVGIYILSSSGDGAXXRDSGS 120
Db 61 VSSSCGPGCHKGTPPTYKEAKQVLSYETLYANGSRTEXQVGIYILSSSGDGAXXRDSGS 120
QY 121 SGKSRKRQIYGYDSRFSIFGKDFLLNYPFSTSVKLSCTGTLVAEXHVLTAACHIDG 180
Db 121 SGKSRKRQIYGYDSRFSIFGKDFLLNYPFSTSVKLSCTGTLVAEXHVLTAACHIDG 180
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; CURRENT APPLICATION NUMBER: US/09/551,826D
; CURRENT FILING DATE: 2000-04-17
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2
; LENGTH: 316
; TYPE: PRT
; ORGANISM: Bacillus licheniformis
US-09-551-826D-2

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Best Local Similarity 23.2%; Pred. No. 4.5e-11;
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QY 120 SSGKSRK-----RQIYGYDSRFSIFGKDFLLNYPFSTSVKLST---GCTGLVAE 167
DB 77 TKEKAEKSPAKAPYSIKSVIGSDRTRVTN---TTAYPYRAIVHISSIGSCTGMMIGP 133
QY 168 XHVLTAACHIHDKT-YVKGTKLRVGLKPKFKDGGRGANDSTSAMPEQMKFQWIRVKR 226
DB 134 KIVATAGHCIIYDTSSGSPAGTATVSPG-----RNGTS-----YPGSVKSTR 175
QY 227 THVPKGIKGNANDIGMDYDIALLEKPKHKFKMKGIVSPPAKQLPGRIHFSGYDNR 286
DB 176 YFIPSGWRSGNTN---YDYGAIELSEPIGNTVGFGYSYTTSLVGTVTITISGYPGDK 230
QY 287 PGNLVYRFGD--VKDETDLLYQQCDAPGASGYGVYVMMKROQKWERKII---GIF 340
DB 231 TAGTQWQHSQPIAISETYKLYQAM-DTYGGQSGSPVFEQSSRTNCSCGCSLAHTNGVY 289
QY 341 SGHQWDMNGSPQDENVAVRITPLKYAQICYW 372
DB 290 GG-----SSYNRGTRITKEVDFNLTNW 311

RESULT 15
US-09-551-826D-10
; Sequence 10, Application US/09551826D
; Patent No. 6558939
; GENERAL INFORMATION:
; APPLICANT: Ostergaard, Peter Rahbek
; APPLICANT: Christensen, Claus Bo Voge
; APPLICANT: Lassen, Soren Flensted
; TITLE OF INVENTION: No. 6558939el Proteases And Variants Thereof
; FILE REFERENCE: 5665.200-US
; CURRENT APPLICATION NUMBER: US/09/551,826D
; CURRENT FILING DATE: 2000-04-17
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 10
; LENGTH: 318
; TYPE: PRT
; ORGANISM: Bacillus licheniformis CDJ31
US-09-551-826D-10

Query Match      7.9%; Score 166; DB 4; Length 318;
Best Local Similarity 23.1%; Pred. No. 4e-09;
Matches 76; Conservative 32; Mismatches 143; Indels 78; Gaps 15;

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QY 120 SSGKSRKQIYGYDSRFSIFGKDFLLNYPFSTSVKLST---GCTGLVAEXHVLTAACH 176
DB 88 PAGPRYSPKSVIGSDRTRVTN---TTAYPYRAIVHISSIGSCTGLIPKTPVATAGHC 144
QY 177 IHD-GKTYVKGTKLRVGLKPKFKDGGRGANDSTSAMPEQMKFQWIRVKRTHVPGWK 235

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; CURRENT APPLICATION NUMBER: US/09/551,826D
; CURRENT FILING DATE: 2000-04-17
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 6
; LENGTH: 314
; TYPE: PRT
; ORGANISM: Bacillus licheniformis AC116
US-09-551-826D-6

Query Match      9.0%; Score 190.5; DB 4; Length 314;
Best Local Similarity 24.4%; Pred. No. 8.9e-12;
Matches 78; Conservative 36; Mismatches 141; Indels 65; Gaps 14;

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QY 123 KSRKQIYGYDSRFSIFGKDFLLNYPFSTSVKLST---GCTGLVAEXHVLTAACHID 179
DB 87 PPSYSPKSVIGSDRTRVTD---TTAPYRAIVHISSIGSCTGLIPKTPVATAGHCYVD 143
QY 180 -GKTYVKGTKLRVGLKPKFKDGGRGANDSTSAMPEQMKFQWIRVKRTHVPKGIKQNA 238
DB 144 TARSFAGTATVSPG-----RNG-----SAYP-----YGSVTSTRYFIPSGWQSGNS 185
QY 239 NDIGMDYDIALLEKPKHKFKMKGIVSPPAKQLPGRIHFSGYDNRPGNLVYRFGD-- 296
DB 186 N-----YDYAAIELSQPIGNTVGFGYSYTTASSLAGAGVTISGYPGDKTTGTQWQSGTI 240
QY 297 VKDETDLLYQQCDAPGASGYGVYVMMKROQKWERKII---GIFSGHQWDMNGSP 352
DB 241 AVSETYKLYQ-AIDTYGGQSGSPVFEKSSRTNCSCGCSLAHTNGVYGG----- 289
QY 353 QDENVAVRITPLKYAQICYW 372
DB 290 SSYNRGTRITKEVDFNFTSW 309

RESULT 14
US-09-551-826D-2
; Sequence 2, Application US/09551826D
; Patent No. 6558939
; GENERAL INFORMATION:
; APPLICANT: No. 6558939regaard-Madsen, Mads
; APPLICANT: Ostergaard, Peter Rahbek
; APPLICANT: Christensen, Claus Bo Voge
; APPLICANT: Lassen, Soren Flensted
; TITLE OF INVENTION: No. 6558939el Proteases And Variants Thereof
; FILE REFERENCE: 5665.200-US

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Db	187	GNSN-----YDYGAIELSQPIGNTVGYFGYSYTTSSLVSSVTIIGYPGDKTSGTQWQMS	241
Qy	288	GNLVYRFGDKDETYDLLYQOCDAQPGASGYGVYVRMWKQKQKWKRII-----GIFSGH	343
Db	242	GNIAV-----SETYKLOY-AIDTYGQSGSPVYEASSRRTNCSGPCSLAVHTNGVYGG-	293
Qy	344	QWDMNGSPQDFNVAVRITPLKYAICYW	372
Db	294	-----SSYNRGTRITKEVFDNLTNW	313

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Job time : 29.5364 secs

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OM protein - protein search, using sw model
Run on: July 1, 2005, 21:08:25 ; Search time 90.3582 Seconds
(without alignments)
1673.692 Million cell updates/sec

Title: US-09-658-677-2
Perfect score: 2112
Sequence: 1 MAGIGLLFLPFLCAVQ.....IKGNLDCREGDTVFLPGSN 392

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5
Searched: 1722976 seqs, 385795295 residues

Total number of hits satisfying chosen parameters: 1722976
Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA:
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2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:
3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:
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11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep:
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22: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2044	96.8	383	9	US-09-765-205-12
2	2044	96.8	383	9	US-09-309-320-261
3	2044	96.8	383	9	US-09-909-088B-261
4	2044	96.8	383	9	US-09-305-291A-261
5	2044	96.8	383	9	US-09-902-853-261
6	2044	96.8	383	9	US-09-907-824-261
7	2044	96.8	383	9	US-09-907-841-261
8	2044	96.8	383	10	US-09-904-011-261
9	2044	96.8	383	10	US-09-903-640-261
10	2044	96.8	383	10	US-09-908-093-261
11	2044	96.8	383	10	US-09-906-742-261
12	2044	96.8	383	10	US-09-906-838-261
13	2044	96.8	383	10	US-09-907-613-261
14	2044	96.8	383	10	US-09-907-942-261
15	2044	96.8	383	10	US-09-904-859-261
16	2044	96.8	383	10	US-09-909-204-261
17	2044	96.8	383	10	US-09-904-820-261
18	2044	96.8	383	10	US-09-904-786-261
19	2044	96.8	383	10	US-09-906-646-261
20	2044	96.8	383	10	US-09-906-700-261
21	2044	96.8	383	10	US-09-903-786-261
22	2044	96.8	383	10	US-09-902-749A-261
23	2044	96.8	383	10	US-09-903-943-261
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35	2044	96.8	383	10	US-09-984-130-126
36	2044	96.8	383	10	US-09-909-064-261
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40	2044	96.8	383	10	US-09-905-348-261
41	2044	96.8	383	10	US-09-905-088-261
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44	2044	96.8	383	10	US-09-902-759-261
45	2044	96.8	383	10	US-09-902-634-261

ALIGNMENTS

RESULT 1
US-09-765-205-12
; Sequence 12, Application US/09765205
; Patent No. US20020034800A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Li
; TITLE OF INVENTION: BONE MARROW SECRETED PROTEINS AND POLYNUCLEOTIDES
; FILE REFERENCE: 1458.004/200130.449
; CURRENT APPLICATION NUMBER: US/09/765,205
; CURRENT FILING DATE: 2001-01-17
; PRIOR APPLICATION NUMBER: US/09/212,440
; PRIOR FILING DATE: 1998-12-16
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 12
; LENGTH: 383
; TYPE: PRT
; ORGANISM: human
; US-09-765-205-12

Query Match 96.8%; Score 2044; DB 9; Length 383;
Best Local Similarity 98.4%; Pred. No. 4e-193; 5; Indels 0; Gaps 0;
Matches 377; Conservative 1; Mismatches 5; Indels 0; Gaps 0;
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Db 1 MAGIGLLFLPFLCAVQVSPYSAPWKPTPAYRLPVVLPQSTLNLAKEPFGAKLE 60
QY 61 VSSSCGPOCHKGTPLPTTYEAKQYLSYETLYANGSTEXQVGIYILSSSGDGAAXRDSGS 120
Db 61 VSSSCGPOCHKGTPLPTTYEAKQYLSYETLYANGSTEXQVGIYILSSSGDGAAXRDSGS 120
QY 121 SKGSRKROIYGVDSRFSIFGKDFLNYFSPSVKLSCTGTLVAEXHVLTAHCIDHG 180

Db 121 SGKSRKRQIYGVDSRFSIFGKDFLLNYPFSTSVKLSGTCTGLVAEKHVLTAACHIDG 180
QY 181 KTYVKGTKLRVGLFKPKDGGGRGANDSTSAMPEQMKFQWIRVKRTHVPKGMWIKGNAND 240
Db 181 KTYVKGTKLRVGLFKPKDGGGRGANDSTSAMPEQMKFQWIRVKRTHVPKGMWIKGNAND 240
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Db 241 IGMDDYDVALLELKPKHKKFKMKIGVSPPAKQLPGGRIFHSGYDNDRPGNLTFRFCVDKDE 300
QY 301 TYDLLYQCCDAQPGASGVGYVYRMMKROQOKWERKIIIGIFSGHQMVDNMGSPQDENVAVR 360
Db 301 TYDLLYQCCDAQPGASGVGYVYRMMKROQOKWERKIIIGIFSGHQMVDNMGSPQDENVAVR 360
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Db 361 ITPLKYAQICYWIKGNLYDCREG 383

RESULT 2
US-09-909-320-261
; Sequence 261, Application US/09909320
; Patent No. US20020132240A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/909,320
; CURRENT FILING DATE: 2002-01-04
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214

; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 261
; LENGTH: 383
; TYPE: PRT
; ORGANISM: Homo Sapien
US-09-909-320-261
Query Match 96.8%; Score 2044; DB 9; Length 383;
Best Local Similarity 98.4%; Pred. No. 4e-193; 5; Indels 0; Gaps 0;
Matches 377; Conservative 1; Mismatches 5; Indels 0; Gaps 0;
QY 1 MAGIFGLLFLFLFLLCAVGVSPYSAPWKPPTWPAVRLPVVLQSTLNLAQPDGAEAKLE 60
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Db 121 SKSRRKQIYGVDSRFSIFGKDFLLNYPFSTSVKLSGTCTGLVAEKHVLTAACHIDG 180
QY 181 KTYVKGTKLRVGLFKPKDGGGRGANDSTSAMPEQMKFQWIRVKRTHVPKGMWIKGNAND 240
Db 181 KTYVKGTKLRVGLFKPKDGGGRGANDSTSAMPEQMKFQWIRVKRTHVPKGMWIKGNAND 240
QY 241 IGMDDYDVALLELKPKHKKFKMKIGVSPPAKQLPGGRIFHSGYDNDRPGNLTFRFCVDKDE 300
Db 241 IGMDDYDVALLELKPKHKKFKMKIGVSPPAKQLPGGRIFHSGYDNDRPGNLTFRFCVDKDE 300
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Db 301 TYDLLYQCCDAQPGASGVGYVYRMMKROQOKWERKIIIGIFSGHQMVDNMGSPQDENVAVR 360
QY 361 ITPLKYAQICYWIKGNLYDCREG 383
Db 361 ITPLKYAQICYWIKGNLYDCREG 383
RESULT 3
US-09-909-088B-261
; Sequence 261, Application US/09909088B
; Patent No. US20020146709A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.

APPLICANT: Grimaldi, Christopher J.
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth, J.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Mather, Jennie P.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: 10466-14
CURRENT APPLICATION NUMBER: US/09/909,088B
PRIOR FILING DATE: 2001-07-18
PRIOR APPLICATION NUMBER: PCT/US00/04414
PRIOR FILING DATE: 2000-02-22
PRIOR APPLICATION NUMBER: US 60/143,048
PRIOR FILING DATE: 1999-07-07
PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR FILING DATE: 1999-07-26
PRIOR APPLICATION NUMBER: US 60/146,222
PRIOR FILING DATE: 1999-07-28
PRIOR APPLICATION NUMBER: PCT/US99/20594
PRIOR FILING DATE: 1999-09-08
PRIOR APPLICATION NUMBER: PCT/US99/20944
PRIOR FILING DATE: 1999-09-13
PRIOR APPLICATION NUMBER: PCT/US99/21090
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/21547
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/23089
PRIOR FILING DATE: 1999-10-05
PRIOR APPLICATION NUMBER: PCT/US99/28214
PRIOR FILING DATE: 1999-11-29
PRIOR APPLICATION NUMBER: PCT/US99/28313
PRIOR FILING DATE: 1999-11-30
PRIOR APPLICATION NUMBER: PCT/US99/28564
PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/28565
PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/30095
PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: PCT/US99/30911
PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US99/30999
PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US00/00219
PRIOR FILING DATE: 2000-01-05
NUMBER OF SEQ ID NOS: 423
SEQ ID NO 261
LENGTH: 383
TYPE: PRT
ORGANISM: Homo Sapien
US-09-909-088B-261

Query Match 96.8%; Score 2044; DB 9; Length 383;
Best Local Similarity 98.4%; Pred. No. 4e-193;
Matches 377; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

Qy 1 MAGIPGLLFLFFLLCAVGQVSPYAPKPTWPAYRLPVVLPQSTLNLAKEPFGAIAKLE 60
Db 1 MAGIPGLLFLFFLLCAVGQVSPYAPKPTWPAYRLPVVLPQSTLNLAKEPFGAIAKLE 60
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Qy 241 IGMVDYALLELKKPHKRFKMGKIGVSPPAKQLPGGRIFHSGYDNDPRGNLVYRFDVKDE 300
Db 241 IGMVDYALLELKKPHKRFKMGKIGVSPPAKQLPGGRIFHSGYDNDPRGNLVYRFDVKDE 300
Qy 301 TYDLLYQCDQAQPGASGYGVYVMMKROQKQKWKRIIGIFSGHQWYDMNGSPQDFNVAVR 360
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Qy 361 ITPKVAQICYWIKNYLDREG 383
Db 361 ITPKVAQICYWIKNYLDREG 383

RESULT 4
US-09-905-291A-261
Sequence 261, Application US/09905291A
Patent No. US20020160374A1
GENERAL INFORMATION:
APPLICANT: Genentech, Inc.
APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, A.
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, Christopher J.
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth, J.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Mather, Jennie P.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: 10466-14
CURRENT APPLICATION NUMBER: US/09/905,291A
CURRENT FILING DATE: 2001-07-12
PRIOR APPLICATION NUMBER: PCT/US00/04414
PRIOR FILING DATE: 2000-02-22
PRIOR APPLICATION NUMBER: US 60/143,048
PRIOR FILING DATE: 1999-07-07
PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR FILING DATE: 1999-07-26
PRIOR APPLICATION NUMBER: US 60/146,222
PRIOR FILING DATE: 1999-07-28
PRIOR APPLICATION NUMBER: PCT/US99/20594
PRIOR FILING DATE: 1999-09-08
PRIOR APPLICATION NUMBER: PCT/US99/20944
PRIOR FILING DATE: 1999-09-13
PRIOR APPLICATION NUMBER: PCT/US99/21090
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/21547
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/23089
PRIOR FILING DATE: 1999-10-05
PRIOR APPLICATION NUMBER: PCT/US99/28214
PRIOR FILING DATE: 1999-11-29

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; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 261
; LENGTH: 383
; TYPE: PRT
; ORGANISM: Homo Sapien
; US-09-905-291A-261

Query Match          96.8%; Score 2044; DB 9; Length 383;
Best Local Similarity 98.4%; Pred. No. 4e-193; 5; Indels 0; Gaps 0;
Matches 377; Conservative 1; Mismatches 0;

QY 1 MAGIPGLLFLFLLCAVGVSPYSAPWKPTWPAYRLPVVLPQSTLNLAKEPFGAEAKLE 60
Db 1 MAGIPGLLFLFLLCAVGVSPYSAPWKPTWPAYRLPVVLPQSTLNLAKEPFGAEAKLE 60
QY 61 VSSSCGPOCHKGTPLPTYEAKQYLSYETLYANGSRTEQVGIYILSSSGDGAXXRDGSG 120
Db 61 VSSSCGPOCHKGTPLPTYEAKQYLSYETLYANGSRTEQVGIYILSSSGDGAXXRDGSG 120
QY 121 SGKSRKRQIYGYDSRFSIFGKDFLNYPESTSVKLSGTCTGLVAEXHVLTAACHIDG 180
Db 121 SGKSRKRQIYGYDSRFSIFGKDFLNYPESTSVKLSGTCTGLVAEXHVLTAACHIDG 180
QY 181 KTVVKGTKLRLVGLFKPKFKDGGRGANDSTAMPEQMKFQIRVKRTHVPKGIKGNAND 240
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Db 361 ITPLKVAQICYKGNVLDREG 383

RESULT 5
US-09-902-853-261
; Sequence 261, Application US/09902853
; Publication No. US20020192659A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnovers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
```

```

; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/902,853
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: US/09/665,350
; PRIOR FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 261
; LENGTH: 383
; TYPE: PRT
; ORGANISM: Homo Sapien
; US-09-902-853-261

Query Match          96.8%; Score 2044; DB 9; Length 383;
Best Local Similarity 98.4%; Pred. No. 4e-193; 5; Indels 0; Gaps 0;
Matches 377; Conservative 1; Mismatches 0;

QY 1 MAGIPGLLFLFLLCAVGVSPYSAPWKPTWPAYRLPVVLPQSTLNLAKEPFGAEAKLE 60
Db 1 MAGIPGLLFLFLLCAVGVSPYSAPWKPTWPAYRLPVVLPQSTLNLAKEPFGAEAKLE 60
QY 61 VSSSCGPOCHKGTPLPTYEAKQYLSYETLYANGSRTEQVGIYILSSSGDGAXXRDGSG 120
Db 61 VSSSCGPOCHKGTPLPTYEAKQYLSYETLYANGSRTEQVGIYILSSSGDGAXXRDGSG 120
QY 121 SGKSRKRQIYGYDSRFSIFGKDFLNYPESTSVKLSGTCTGLVAEXHVLTAACHIDG 180
Db 121 SGKSRKRQIYGYDSRFSIFGKDFLNYPESTSVKLSGTCTGLVAEXHVLTAACHIDG 180
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Qy	181	KTYVKGTKLAVGFLKPKFKOGGRGANDESTAMPEQMKEPQWIRVRKETHVPKGIWIGNAND	240
Dd	181	KTYVKGTKLAVGFLKPKFKOGGRGANDESTAMPEQMKEPQWIRVRKETHVPKGIWIGNAND	240
Qy	241	IGMDYDALLLEKKPHKPKFMKI GVSPPAKQLPGGRIHFSGVDNDRPGNLVTRFCVDKDE	300
Dd	241	IGMDYDALLLEKKPHKPKFMKI GVSPPAKQLPGGRIHFSGVDNDRPGNLVTRFCVDKDE	300
Qy	301	TYDLLYQQCDAPQASGGYGVVYRWVKRQQKWERKI IGFSGHQWDMNGSPQDFNVAYR	360
Dd	301	TYDLLYQQCDAPQASGGYGVVYRWVKRQQKWERKI IGFSGHQWDMNGSPQDFNVAYR	360
Qy	361	ITPLKYAQICYWIKNGYLDCCREG	383
Dd	361	ITPLKYAQICYWIKNGYLDCCREG	383

RESULT 6

US-09-907-824-261

Sequence 261, Application US/09907824

Publication No. US20020197671A1

GENERAL INFORMATION:

APPLICANT: Genentech, Inc.

APPLICANT: Ashkenazi, Avi

APPLICANT: Botstein, David

APPLICANT: Desnoyers, Luc

APPLICANT: Eaton, Dan L.

APPLICANT: Ferrara, Napoleone

APPLICANT: Filvaroff, Ellen

APPLICANT: Fong, Sherman

APPLICANT: Gao, Wei-Qiang

APPLICANT: Gerber, Hanspeter

APPLICANT: Gerritsen, Mary E.

APPLICANT: Goddard, A.

APPLICANT: Godowski, Paul J.

APPLICANT: Grimaldi, Christopher J.

APPLICANT: Gurney, Austin L.

APPLICANT: Hillan, Kenneth, J.

APPLICANT: Kljavin, Ivar J.

APPLICANT: Mather, Jennie P.

APPLICANT: Pan, James

APPLICANT: Paoni, Nicholas F.

APPLICANT: Roy, Margaret Ann

APPLICANT: Stewart, Timothy A.

APPLICANT: Tuma, Daniel

APPLICANT: Williams, P. Mickey

APPLICANT: Wood, William, I.

TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic Acids Encoding the Same

FILE REFERENCE: 10466-14

CURRENT APPLICATION NUMBER: US/09/907,824

PRIOR FILING DATE: 2001-07-17

PRIOR APPLICATION NUMBER: 09/665,350

PRIOR FILING DATE: 2000-09-18

PRIOR APPLICATION NUMBER: PCT/US00/04414

PRIOR FILING DATE: 2000-02-22

PRIOR APPLICATION NUMBER: US 60/143,048

PRIOR FILING DATE: 1999-07-07

PRIOR APPLICATION NUMBER: US 60/145,698

PRIOR FILING DATE: 1999-07-26

PRIOR APPLICATION NUMBER: US 60/146,222

PRIOR FILING DATE: 1999-07-28

PRIOR APPLICATION NUMBER: PCT/US99/20594

PRIOR FILING DATE: 1999-09-08

PRIOR APPLICATION NUMBER: PCT/US99/20944

PRIOR FILING DATE: 1999-09-13

PRIOR APPLICATION NUMBER: PCT/US99/21090

PRIOR FILING DATE: 1999-09-15

PRIOR APPLICATION NUMBER: PCT/US99/21547

PRIOR FILING DATE: 1999-09-15

PRIOR APPLICATION NUMBER: PCT/US99/23089

PRIOR FILING DATE: 1999-10-05

PRIOR APPLICATION NUMBER: PCT/US99/28214

[illegible]

RESIN, T 7

US-09-907-841-261
Sequence 261, Application US/09907841
Publication No. US20020198366A1
GENERAL INFORMATION:
APPLICANT: Genentech, Inc.
APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
APPLICANT: Desnuyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gertschen, Mary E.
APPLICANT: Goddard, A.
APPLICANT: Godowski, Paul J.

APPLICANT: Grimaldi, Christopher J.
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth, J.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Mather, Jennie P.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: 10466-14
CURRENT APPLICATION NUMBER: US/09/907,841
PRIOR APPLICATION NUMBER: PCT/US00/04414
PRIOR FILING DATE: 2000-02-22
PRIOR APPLICATION NUMBER: US 60/143,048
PRIOR FILING DATE: 1999-07-07
PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR FILING DATE: 1999-07-26
PRIOR APPLICATION NUMBER: US 60/146,222
PRIOR FILING DATE: 1999-07-28
PRIOR APPLICATION NUMBER: PCT/US99/20594
PRIOR FILING DATE: 1999-09-08
PRIOR APPLICATION NUMBER: PCT/US99/20944
PRIOR FILING DATE: 1999-09-13
PRIOR APPLICATION NUMBER: PCT/US99/21090
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/21547
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/23089
PRIOR FILING DATE: 1999-10-05
PRIOR APPLICATION NUMBER: PCT/US99/28214
PRIOR FILING DATE: 1999-11-29
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 423
SEQ ID NO 261
LENGTH: 393
TYPE: PRT
ORGANISM: Homo Sapien
US-09-907-841-261

Query Match 96.8%; Score 2044; DB 9; Length 383;
Best Local Similarity 98.4%; Pred. No. 4e-193;
Matches 377; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

Qy 1 MAGIPGLFLLFLLCAVGQVSPYSAPWKTWPAYRLPVVLPQSTLNLAQDFGAEAKLE 60
Db 1 MAGIPGLFLLFLLCAVGQVSPYSAPWKTWPAYRLPVVLPQSTLNLAQDFGAEAKLE 60

Qy 61 VSSSCGPOCHKGTPLPTYKAKQVLSYETLYANGSRTEKXQVGIYILSSGSGAXRDSGS 120
Db 61 VSSSCGPOCHKGTPLPTYKAKQVLSYETLYANGSRTEKXQVGIYILSSGSGAXRDSGS 120

Qy 121 SGSRKRQIYGVDSRFSIFGKDFLLNYPSTSVKLTGCTGTVAEXHVLTAACHIDG 180
Db 121 SGSRKRQIYGVDSRFSIFGKDFLLNYPSTSVKLTGCTGTVAEXHVLTAACHIDG 180

Qy 181 KTVVGTQKLRVGLFKPKFDGGRGANDSTSAMPEQMKFQWIRVKTHTVPKGIKGNAND 240
Db 181 KTVVGTQKLRVGLFKPKFDGGRGANDSTSAMPEQMKFQWIRVKTHTVPKGIKGNAND 240

Qy 241 IGMDDYVALLLEKKPKRKPWKVGVSPAPKALPGGRIFHSGYNDPRGNLVYRFDVKDE 300
Db 241 IGMDDYVALLLEKKPKRKPWKVGVSPAPKALPGGRIFHSGYNDPRGNLVYRFDVKDE 300

Qy 301 TYDLLYQCDAPQACSGGVYVVRWKQKQKWERKLIIGFSGHQWDMNGSPQDENVAVR 360
Db 301 TYDLLYQCDAPQACSGGVYVVRWKQKQKWERKLIIGFSGHQWDMNGSPQDENVAVR 360

Qy 361 ITPLKYAQICYWIKGNYLDCREG 383
Db 361 ITPLKYAQICYWIKGNYLDCREG 383

RESULT 8
US-09-904-011-261
Sequence 261, Application US/09904011
Publication No. US2003000350A1
GENERAL INFORMATION:
APPLICANT: Genentech, Inc.
APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, A.
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, Christopher J.
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth, J.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Mather, Jennie P.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: 10466-14
CURRENT APPLICATION NUMBER: US/09/904,011
CURRENT FILING DATE: 2001-07-11
PRIOR APPLICATION NUMBER: 09/665,350
PRIOR FILING DATE: 2000-09-18
PRIOR APPLICATION NUMBER: PCT/US00/04414
PRIOR FILING DATE: 2000-02-22
PRIOR APPLICATION NUMBER: US 60/143,048
PRIOR FILING DATE: 1999-07-07
PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR FILING DATE: 1999-07-26
PRIOR APPLICATION NUMBER: US 60/146,222
PRIOR FILING DATE: 1999-07-28
PRIOR APPLICATION NUMBER: PCT/US99/20594
PRIOR FILING DATE: 1999-09-08
PRIOR APPLICATION NUMBER: PCT/US99/20944
PRIOR FILING DATE: 1999-09-13
PRIOR APPLICATION NUMBER: PCT/US99/21090
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/21547
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/23089
PRIOR FILING DATE: 1999-10-05
PRIOR APPLICATION NUMBER: PCT/US99/28214
PRIOR FILING DATE: 1999-11-29
PRIOR APPLICATION NUMBER: PCT/US99/28313
PRIOR FILING DATE: 1999-11-30
PRIOR APPLICATION NUMBER: PCT/US99/28564
PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/28565
PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/30095
PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: PCT/US99/30911
PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US99/30999

; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 261
; LENGTH: 383
; TYPE: PRT
; ORGANISM: Homo Sapien
US-09-904-011-261

Query Match 96.8%; Score 2044; DB 10; Length 383;
Best Local Similarity 98.4%; Pred. No. 4e-193;
Matches 377; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 1 MAGIPGLLLFLLFLLCAVGQVSPYSAPWKPTWPAAYRLPVVLPQSTLNLAKEPFGAEAKLE 60
DB 1 MAGIPGLLLFLLFLLCAVGQVSPYSAPWKPTWPAAYRLPVVLPQSTLNLAKEPFGAEAKLE 60

QY 61 VSSSCGPQCHKGTPLPTYEAKQYLSYETLYANGSRTEXQVGIYILSSSGDGAXXRDSGS 120
DB 61 VSSSCGPQCHKGTPLPTYEAKQYLSYETLYANGSRTEXQVGIYILSSSGDGAXXRDSGS 120

QY 121 SGKSRKRQIYGVDSRFSIFGKDFLLNYPFSTSVKLSGTGTLVAEXHVLTAACHIDG 180
DB 121 SGKSRKRQIYGVDSRFSIFGKDFLLNYPFSTSVKLSGTGTLVAEXHVLTAACHIDG 180

QY 181 KTVYKGTQKLRVGLFKPKFGDGGRGANDSTSAMPEQMKFQWIRVKTTHVPKGIKGNAND 240
DB 181 KTVYKGTQKLRVGLFKPKFGDGGRGANDSTSAMPEQMKFQWIRVKTTHVPKGIKGNAND 240

QY 241 IGMDDYVALLLEKKPHKFKMKIGVSPPAKQLPGRIHFSGYNDNDRPGNLVYRFDVKDE 300
DB 241 IGMDDYVALLLEKKPHKFKMKIGVSPPAKQLPGRIHFSGYNDNDRPGNLVYRFDVKDE 300

QY 301 TYDLLYQQCDAQPGASGYGVYVVMWKQKQKWERKIIGIFSGHQWDMNGSPQDFNVAVR 360
DB 301 TYDLLYQQCDAQPGASGYGVYVVMWKQKQKWERKIIGIFSGHQWDMNGSPQDFNVAVR 360

RESULT 9

US-09-903-640-261
; Sequence 261, Application US/09903640
; Publication No. US20030017463A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnovers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.

; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/903,640
; CURRENT FILING DATE: 2001-07-11
; PRIOR APPLICATION NUMBER: 09/665,350
; PRIOR FILING DATE: 2000-09-18
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 261
; LENGTH: 383
; TYPE: PRT
; ORGANISM: Homo Sapien
US-09-903-640-261

Query Match 96.8%; Score 2044; DB 10; Length 383;
Best Local Similarity 98.4%; Pred. No. 4e-193;
Matches 377; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 1 MAGIPGLLLFLLFLLCAVGQVSPYSAPWKPTWPAAYRLPVVLPQSTLNLAKEPFGAEAKLE 60
DB 1 MAGIPGLLLFLLFLLCAVGQVSPYSAPWKPTWPAAYRLPVVLPQSTLNLAKEPFGAEAKLE 60

QY 61 VSSSCGPQCHKGTPLPTYEAKQYLSYETLYANGSRTEXQVGIYILSSSGDGAXXRDSGS 120
DB 61 VSSSCGPQCHKGTPLPTYEAKQYLSYETLYANGSRTEXQVGIYILSSSGDGAXXRDSGS 120

QY 121 SGKSRKRQIYGVDSRFSIFGKDFLLNYPFSTSVKLSGTGTLVAEXHVLTAACHIDG 180
DB 121 SGKSRKRQIYGVDSRFSIFGKDFLLNYPFSTSVKLSGTGTLVAEXHVLTAACHIDG 180

QY 181 KTVYKGTQKLRVGLFKPKFGDGGRGANDSTSAMPEQMKFQWIRVKTTHVPKGIKGNAND 240
DB 181 KTVYKGTQKLRVGLFKPKFGDGGRGANDSTSAMPEQMKFQWIRVKTTHVPKGIKGNAND 240

QY 241 IGMDDYVALLLEKKPHKFKMKIGVSPPAKQLPGRIHFSGYNDNDRPGNLVYRFDVKDE 300
DB 241 IGMDDYVALLLEKKPHKFKMKIGVSPPAKQLPGRIHFSGYNDNDRPGNLVYRFDVKDE 300

QY 301 TYDLLYQQCDAQPGASGYGVYVVMWKQKQKWERKIIGIFSGHQWDMNGSPQDFNVAVR 360
DB 301 TYDLLYQQCDAQPGASGYGVYVVMWKQKQKWERKIIGIFSGHQWDMNGSPQDFNVAVR 360

QY 361 ITPLKYAQICYWIKGNLYDCREG 383
DB 361 ITPLKYAQICYWIKGNLYDCREG 383

RESULT 10

US-09-908-093-261
; Sequence 261, Application US/09908093
; Publication No. US20030017498A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnovers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann

```

; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/908,093
; CURRENT FILING DATE: 2001-07-17
; PRIOR FILING DATE: 2001-07-17
; PRIOR FILING DATE: 2000-09-18
; PRIOR FILING DATE: 2000-09-18
; PRIOR FILING DATE: 2000-02-22
; PRIOR FILING DATE: 1999-07-07
; PRIOR FILING DATE: 1999-07-07
; PRIOR FILING DATE: 1999-07-26
; PRIOR FILING DATE: 1999-07-26
; PRIOR FILING DATE: 1999-07-28
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; PRIOR FILING DATE: 1999-09-15
; PRIOR FILING DATE: 1999-10-05
; PRIOR FILING DATE: 1999-10-05
; PRIOR FILING DATE: 1999-11-29
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; PRIOR FILING DATE: 1999-11-30
; PRIOR FILING DATE: 1999-11-30
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; PRIOR FILING DATE: 1999-12-02
; PRIOR FILING DATE: 1999-12-02
; PRIOR FILING DATE: 1999-12-02
; PRIOR FILING DATE: 1999-12-16
; PRIOR FILING DATE: 1999-12-16
; PRIOR FILING DATE: 1999-12-20
; PRIOR FILING DATE: 1999-12-20
; PRIOR FILING DATE: 1999-12-20
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 261
; LENGTH: 383
; TYPE: PRT
; ORGANISM: Homo Sapien
US-09-908-093-261

Query Match          96.8%; Score 2044; DB 10; Length 383;
Best Local Similarity 98.4%; Pred. No. 4e-193;
Matches 377; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 1 MAGIPGLLFLFLLCAGVGQSPVSPAPKPTWPAYRLPVVLPQSTLNLAKEPFGAEAKLE 60
DB 1 MAGIPGLLFLFLLCAGVGQSPVSPAPKPTWPAYRLPVVLPQSTLNLAKEPFGAEAKLE 60
QY 61 VSSSCGPGCHKGTPLTPTYPEAKQYLSYETLYANGSRTEKXQVGIYIILSSSGDGAXRDSGS 120
DB 61 VSSSCGPGCHKGTPLTPTYPEAKQYLSYETLYANGSRTEKXQVGIYIILSSSGDGAXRDSGS 120
QY 121 SGKSRKRQIYGVDSRFSIFGKDFLLNYPFSTSVKLTGCTGLTVAEXHVLTAACHIHOG 180
DB 121 SGKSRKRQIYGVDSRFSIFGKDFLLNYPFSTSVKLTGCTGLTVAEXHVLTAACHIHOG 180
QY 181 KTVVKGTKLVRGLFKPKPGDGRGNDSTSAMPEQMKFQWIRVKRTHVPKGIKGNAND 240
DB 181 KTVVKGTKLVRGLFKPKPGDGRGNDSTSAMPEQMKFQWIRVKRTHVPKGIKGNAND 240
QY 241 IGMDDYDALLELEKPKHKKPMKIGVSPPAKQLPGGRIHFSGYDNDPRGNLVRFCVDKDE 300
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DB 241 IGMDDYDALLELEKPKHKKPMKIGVSPPAKQLPGGRIHFSGYDNDPRGNLVRFCVDKDE 300
QY 301 TYDLLYQQCDAOPGASGVYVVRMMKROQKWKERKIIGIFSGHQWVDMMNGSPQDENAVR 360
DB 301 TYDLLYQQCDAOPGASGVYVVRMMKROQKWKERKIIGIFSGHQWVDMMNGSPQDENAVR 360
QY 361 ITPLKYAQICYWIKGNLYDCREG 383
DB 361 ITPLKYAQICYWIKGNLYDCREG 383

RESULT 11
US-09-906-742-261
; Sequence 261, Application US/09906742
; Publication No. US20030023054A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/906,742
; CURRENT FILING DATE: 2001-07-16
; PRIOR APPLICATION NUMBER: 09/665,350
; PRIOR FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
```

; PRIOR APPLICATION NUMBER: PCT/US99/28565
 ; PRIOR FILING DATE: 1999-12-02
 ; PRIOR APPLICATION NUMBER: PCT/US99/30095
 ; PRIOR FILING DATE: 1999-12-16
 ; PRIOR APPLICATION NUMBER: PCT/US99/30911
 ; PRIOR FILING DATE: 1999-12-20
 ; PRIOR APPLICATION NUMBER: PCT/US99/30999
 ; PRIOR FILING DATE: 1999-12-20
 ; PRIOR APPLICATION NUMBER: PCT/US00/00219
 ; PRIOR FILING DATE: 2000-01-05
 ; NUMBER OF SEQ ID NOS: 423
 ; SEQ ID NO 261
 ; LENGTH: 383
 ; TYPE: PRT
 ; ORGANISM: Homo Sapien
 US-09-906-742-261

Query Match 96.8%; Score 2044; DB 10; Length 383;

Best Local Similarity 98.4%; Pred. No. 4e-193;

Matches 377; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY	1	MAGIPGLLFLFLCAVGVSPYSAPWKTWPAYRLPVVLPQSTLNLAKEPFGAEAKLE	60
Db	1	MAGIPGLLFLFLCAVGVSPYSAPWKTWPAYRLPVVLPQSTLNLAKEPFGAEAKLE	60
QY	61	VSSSCGPGCHKTPLPTTYKEAKOYLSYETLYANGSRTEXOVGIYILSSSGDGAXXRDSGS	120
Db	61	VSSSCGPGCHKTPLPTTYKEAKOYLSYETLYANGSRTEXOVGIYILSSSGDGAXXRDSGS	120
QY	121	SGKSRKRQIYGYDSRFSIFGKDFLLNYPSTSVKLSGTCTGLVAEXHVLTAACHIDG	180
Db	121	SGKSRKRQIYGYDSRFSIFGKDFLLNYPSTSVKLSGTCTGLVAEXHVLTAACHIDG	180
QY	181	KTVYKGTQKLRVGLFKPKFKDGGGRANDSTAMPEQMKFQIRVKTHTVPKGIKGNAND	240
Db	181	KTVYKGTQKLRVGLFKPKFKDGGGRANDSTAMPEQMKFQIRVKTHTVPKGIKGNAND	240
QY	241	IGMDYDVALLELKKPKKPKWKIGVSPKOLGGRIFHSYDNDPRGNLVPFCVDKDE	300
Db	241	IGMDYDVALLELKKPKKPKWKIGVSPKOLGGRIFHSYDNDPRGNLVPFCVDKDE	300
QY	301	TYDLLVQCCDAQPGASGYGVYVVMKRRQKQKWKIIGIFSGHQWDMNGSPQDFNVAVR	360
Db	301	TYDLLVQCCDAQPGASGYGVYVVMKRRQKQKWKIIGIFSGHQWDMNGSPQDFNVAVR	360
QY	361	ITPLKVAICYWIKGNVLDREG	383
Db	361	ITPLKVAICYWIKGNVLDREG	383

RESULT 12

US-09-906-838-261
 ; Sequence 261, Application US/09906838
 ; Publication No. US20030027143A1
 ; GENERAL INFORMATION:

; APPLICANT: Genentech, Inc.
 ; APPLICANT: Ashkenazi, Avi
 ; APPLICANT: Botstein, David
 ; APPLICANT: Desnoyers, Luc
 ; APPLICANT: Eaton, Dan L.
 ; APPLICANT: Ferrara, Napoleone
 ; APPLICANT: Filvaroff, Ellen
 ; APPLICANT: Fong, Sherman
 ; APPLICANT: Gao, Wei-Qiang
 ; APPLICANT: Gerber, Hanspeter
 ; APPLICANT: Gerritsen, Mary E.
 ; APPLICANT: Goddard, A.
 ; APPLICANT: Godowski, Paul J.
 ; APPLICANT: Grimaldi, Christopher J.
 ; APPLICANT: Gurney, Austin L.
 ; APPLICANT: Hillan, Kenneth, J.
 ; APPLICANT: Kljavin, Ivar J.
 ; APPLICANT: Mather, Jennie P.

; APPLICANT: Pan, James
 ; APPLICANT: Paoni, Nicholas F.
 ; APPLICANT: Roy, Margaret Ann
 ; APPLICANT: Stewart, Timothy A.
 ; APPLICANT: Tumas, Daniel
 ; APPLICANT: Williams, P. Mickey
 ; APPLICANT: Wood, William, I.

; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
 ; FILE REFERENCE: 10466-14
 ; CURRENT APPLICATION NUMBER: US/09/906,838
 ; CURRENT FILING DATE: 2001-07-16
 ; PRIOR APPLICATION NUMBER: 09/665,350
 ; PRIOR FILING DATE: 2000-09-18
 ; PRIOR APPLICATION NUMBER: PCT/US00/04414
 ; PRIOR FILING DATE: 2000-02-22
 ; PRIOR APPLICATION NUMBER: US 60/143,048
 ; PRIOR FILING DATE: 1999-07-07
 ; PRIOR APPLICATION NUMBER: US 60/145,698
 ; PRIOR FILING DATE: 1999-07-26
 ; PRIOR APPLICATION NUMBER: US 60/146,222
 ; PRIOR FILING DATE: 1999-07-28
 ; PRIOR APPLICATION NUMBER: PCT/US99/20594
 ; PRIOR FILING DATE: 1999-09-08
 ; PRIOR APPLICATION NUMBER: PCT/US99/20944
 ; PRIOR FILING DATE: 1999-09-13
 ; PRIOR APPLICATION NUMBER: PCT/US99/21090
 ; PRIOR FILING DATE: 1999-09-15
 ; PRIOR APPLICATION NUMBER: PCT/US99/21547
 ; PRIOR FILING DATE: 1999-09-15
 ; PRIOR APPLICATION NUMBER: PCT/US99/23089
 ; PRIOR FILING DATE: 1999-10-05
 ; PRIOR APPLICATION NUMBER: PCT/US99/28214
 ; PRIOR FILING DATE: 1999-11-29
 ; PRIOR APPLICATION NUMBER: PCT/US99/28313
 ; PRIOR FILING DATE: 1999-11-30
 ; PRIOR APPLICATION NUMBER: PCT/US99/28564
 ; PRIOR FILING DATE: 1999-12-02
 ; PRIOR APPLICATION NUMBER: PCT/US99/28565
 ; PRIOR FILING DATE: 1999-12-02
 ; PRIOR APPLICATION NUMBER: PCT/US99/30095
 ; PRIOR FILING DATE: 1999-12-16
 ; PRIOR APPLICATION NUMBER: PCT/US99/30911
 ; PRIOR FILING DATE: 1999-12-20
 ; PRIOR APPLICATION NUMBER: PCT/US99/30999
 ; PRIOR FILING DATE: 1999-12-20
 ; PRIOR APPLICATION NUMBER: PCT/US00/00219
 ; PRIOR FILING DATE: 2000-01-05
 ; NUMBER OF SEQ ID NOS: 423
 ; SEQ ID NO 261
 ; LENGTH: 383
 ; TYPE: PRT
 ; ORGANISM: Homo Sapien
 US-09-906-838-261

Query Match 96.8%; Score 2044; DB 10; Length 383;

Best Local Similarity 98.4%; Pred. No. 4e-193;

Matches 377; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY	1	MAGIPGLLFLFLCAVGVSPYSAPWKTWPAYRLPVVLPQSTLNLAKEPFGAEAKLE	60
Db	1	MAGIPGLLFLFLCAVGVSPYSAPWKTWPAYRLPVVLPQSTLNLAKEPFGAEAKLE	60
QY	61	VSSSCGPGCHKTPLPTTYKEAKOYLSYETLYANGSRTEXOVGIYILSSSGDGAXXRDSGS	120
Db	61	VSSSCGPGCHKTPLPTTYKEAKOYLSYETLYANGSRTEXOVGIYILSSSGDGAXXRDSGS	120
QY	121	SGKSRKRQIYGYDSRFSIFGKDFLLNYPSTSVKLSGTCTGLVAEXHVLTAACHIDG	180
Db	121	SGKSRKRQIYGYDSRFSIFGKDFLLNYPSTSVKLSGTCTGLVAEXHVLTAACHIDG	180
QY	181	KTVYKGTQKLRVGLFKPKFKDGGGRANDSTAMPEQMKFQIRVKTHTVPKGIKGNAND	240

Db 181 KTYVKGTKLRVGLFKPKFKDGGGRGANDSTSAMPEQMKFQWIRVXKTHVPGKWKGNAND 240
Qy 241 IGWDYDVALLELKKPKKFKMGKIGVSPAKQLPGRIHFSGYDNDPRGNLVYRFCVDKDE 300
Db 241 IGWDYDVALLELKKPKKFKMGKIGVSPAKQLPGRIHFSGYDNDPRGNLVYRFCVDKDE 300
Qy 301 TYDLYQQCDAQPGASGYVYVMWKRQOQKWERKIIIGIFSGHQWYDMNGSPQDFNVAVR 360
Db 301 TYDLYQQCDAQPGASGYVYVMWKRQOQKWERKIIIGIFSGHQWYDMNGSPQDFNVAVR 360
Qy 361 ITPLKYAQICYWIKGNLYDCREG 383
Db 361 ITPLKYAQICYWIKGNLYDCREG 383

RESULT 13

US-09-907-613-261
; Sequence 261, Application US/09907613
; Publication No. US20030027145A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, David
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kijavlin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/907,613
; CURRENT FILING DATE: 2001-07-17
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564

; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 261
; LENGTH: 383
; TYPE: PRT
; ORGANISM: Homo Sapien
US-09-907-613-261
Query Match 96.8%; Score 2044; DB 10; Length 383;
Best Local Similarity 98.4%; Pred. No. 4e-193;
Matches 377; Conservative 1; Mismatches 5; Indels 0; Gaps 0;
Qy 1 MAGIFGLLELFLFLLCAVQNSPYSPAPKPTWPAYRLPVVLPOSTLNLAKEPFGAEAKLE 60
Db 1 MAGIFGLLELFLFLLCAVQNSPYSPAPKPTWPAYRLPVVLPOSTLNLAKEPFGAEAKLE 60
Qy 61 VSSSCGPOCHKGTPLPTYKAKQYLSYETLYANGSRTEXQVGIYILSSSGDGAXXRDSGS 120
Db 61 VSSSCGPOCHKGTPLPTYEAKQYLSYETLYANGSRTEXQVGIYILSSSGDGAXXRDSGS 120
Qy 121 SGKRRKRQIYGYDSRFSIFGKDFLLNYPFSTSVKLSTGCTCTLVAEXHVLTAACHIDG 180
Db 121 SGKRRKRQIYGYDSRFSIFGKDFLLNYPFSTSVKLSTGCTCTLVAEXHVLTAACHIDG 180
Qy 181 KTYVKGTKLRVGLFKPKFKDGGGRGANDSTSAMPEQMKFQWIRVXKTHVPGKWKGNAND 240
Db 181 KTYVKGTKLRVGLFKPKFKDGGGRGANDSTSAMPEQMKFQWIRVXKTHVPGKWKGNAND 240
Qy 241 IGWDYDVALLELKKPKKFKMGKIGVSPAKQLPGRIHFSGYDNDPRGNLVYRFCVDKDE 300
Db 241 IGWDYDVALLELKKPKKFKMGKIGVSPAKQLPGRIHFSGYDNDPRGNLVYRFCVDKDE 300
Qy 301 TYDLYQQCDAQPGASGYVYVMWKRQOQKWERKIIIGIFSGHQWYDMNGSPQDFNVAVR 360
Db 301 TYDLYQQCDAQPGASGYVYVMWKRQOQKWERKIIIGIFSGHQWYDMNGSPQDFNVAVR 360
Qy 361 ITPLKYAQICYWIKGNLYDCREG 383
Db 361 ITPLKYAQICYWIKGNLYDCREG 383

RESULT 14

US-09-907-942-261
; Sequence 261, Application US/09907942
; Publication No. US20030027146A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, David
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kijavlin, Ivar J.

APPLICANT: Mather, Jennie P.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: 10466-14
CURRENT APPLICATION NUMBER: US/09/907,942
CURRENT FILING DATE: 2002-01-22
PRIOR APPLICATION NUMBER: PCT/US00/04414
PRIOR FILING DATE: 2000-02-22
PRIOR APPLICATION NUMBER: US 60/143,048
PRIOR FILING DATE: 1999-07-07
PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR FILING DATE: 1999-07-26
PRIOR APPLICATION NUMBER: US 60/146,222
PRIOR FILING DATE: 1999-07-28
PRIOR APPLICATION NUMBER: PCT/US99/20594
PRIOR FILING DATE: 1999-09-08
PRIOR APPLICATION NUMBER: PCT/US99/20944
PRIOR FILING DATE: 1999-09-13
PRIOR APPLICATION NUMBER: PCT/US99/21090
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/21547
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/23089
PRIOR FILING DATE: 1999-10-05
PRIOR APPLICATION NUMBER: PCT/US99/28214
PRIOR FILING DATE: 1999-11-29
PRIOR APPLICATION NUMBER: PCT/US00/00219
PRIOR FILING DATE: 2000-01-05
NUMBER OF SEQ ID NOS: 423
SEQ ID NO 261
LENGTH: 383
TYPE: PRT
ORGANISM: Homo Sapien
US-09-907-942-261

Query Match 96.8%; Score 2044; DB 10; Length 383;
Best Local Similarity 98.4%; Pred. No. 4e-193;
Matches 377; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

Qy 1 MAGIPGLLFLFFLLCAVGQSPYSAPWKPTWPAYRLPVVLPQSTLNLAKEPFGAEAKLE 60
Db 1 MAGIPGLLFLFFLLCAVGQSPYSAPWKPTWPAYRLPVVLPQSTLNLAKEPFGAEAKLE 60

Qy 61 VSSSCGQCHKGTPLPYKAKQVLSYETLYANGSRTEXQVGIYILSSGSGDGAAXRDSGS 120
Db 61 VSSSCGQCHKGTPLPYKAKQVLSYETLYANGSRTEXQVGIYILSSGSGDGAAXRDSGS 120

Qy 121 SGKSRKQIYGVDSRESIFGKQFLNYPSTSVKLSGTCTGLVAEXHVLTAACHIDG 180
Db 121 SGKSRKQIYGVDSRESIFGKQFLNYPSTSVKLSGTCTGLVAEXHVLTAACHIDG 180

Qy 181 KTVYKGTQKLRVGLFKPKFGDGGREGANDSAMPQMKFQWIRKRVTHVPKGIKGNAND 240
Db 181 KTVYKGTQKLRVGLFKPKFGDGGREGANDSAMPQMKFQWIRKRVTHVPKGIKGNAND 240

Qy 241 IGMDDYALLELAKKPHKRFKMGIVSPPAKQLPGRIHFSGYDNRGNLVYRFDVKDE 300
Db 241 IGMDDYALLELAKKPHKRFKMGIVSPPAKQLPGRIHFSGYDNRGNLVYRFDVKDE 300

Qy 301 TYDLLYQQCDAPGASGYGVYVRMWRQKQKWKRIIGFSGHQWVDMNGSPQDFNVAVR 360
Db 301 TYDLLYQQCDAPGASGYGVYVRMWRQKQKWKRIIGFSGHQWVDMNGSPQDFNVAVR 360

Qy 361 ITPLKYAQICYWIKGNLYDCREG 383
Db 361 ITPLKYAQICYWIKGNLYDCREG 383

RESULT 15
US-09-904-859-261
Sequence 261, Application US/09904859
Publication No. US2003003060A1
GENERAL INFORMATION:
APPLICANT: Genentech, Inc.
APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
APPLICANT: Deenoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, A.
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, Christopher J.
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth, J.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Mather, Jennie P.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: 10466-14
CURRENT APPLICATION NUMBER: US/09/904,859
CURRENT FILING DATE: 2001-07-12
PRIOR APPLICATION NUMBER: 09/665,350
PRIOR FILING DATE: 2000-09-18
PRIOR APPLICATION NUMBER: PCT/US00/04414
PRIOR FILING DATE: 2000-02-22
PRIOR APPLICATION NUMBER: US 60/143,048
PRIOR FILING DATE: 1999-07-07
PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR FILING DATE: 1999-07-26
PRIOR APPLICATION NUMBER: US 60/146,222
PRIOR FILING DATE: 1999-07-28
PRIOR APPLICATION NUMBER: PCT/US99/20594
PRIOR FILING DATE: 1999-09-08
PRIOR APPLICATION NUMBER: PCT/US99/20944
PRIOR FILING DATE: 1999-09-13
PRIOR APPLICATION NUMBER: PCT/US99/21090
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/21547
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/23089
PRIOR FILING DATE: 1999-10-05
PRIOR APPLICATION NUMBER: PCT/US99/28214
PRIOR FILING DATE: 1999-11-29
PRIOR APPLICATION NUMBER: PCT/US99/28313
PRIOR FILING DATE: 1999-11-30

; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 261
; LENGTH: 383
; TYPE: PRT
; ORGANISM: Homo Sapien
US-09-904-859-261

Query Match 96.8%; Score 2044; DB 10; Length 383;
Best Local Similarity 98.4%; Pred. No. 4e-193;
Matches 377; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

Qy 1 MAGTGGLLFLFLCAVGVSPYSAPWKETWPAAYRLPVVLPOSTLNIAKPDFGAEAKLE 60
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1 MAGTGGLLFLFLCAVGVSPYSAPWKETWPAAYRLPVVLPOSTLNIAKPDFGAEAKLE 60

Qy 61 VSSSCGPGCHKGTPPTYKEAKQVLSYETLYANGSRTEXQVGIYIILSSGDXRDSGS 120
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
61 VSSSCGPGCHKGTPPTYEAKQVLSYETLYANGSRTEXQVGIYIILSSGDXRDSGS 120

Qy 121 SGKSRKRQIYGYDSRFSIFGKDFLLNYPFSTSVKLSTGCTGLVAEXHVLTAACHIDG 180
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
121 SGKSRKRQIYGYDSRFSIFGKDFLLNYPFSTSVKLSTGCTGLVAEXHVLTAACHIDG 180

Qy 181 KTVYKGTQKLVGFLKPKFYDGGRGANDSTSAMPEQMKFQWIRVKTHTVPKGIKGNAND 240
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
181 KTVYKGTQKLVGFLKPKFYDGGRGANDSTSAMPEQMKFQWIRVKTHTVPKGIKGNAND 240

Qy 241 IGMDYDVALLELKKPHKPKMKIGVSPPAKQLPGGRIFHSGYDNDPRGNLVYRFCVDKDE 300
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
241 IGMDYDVALLELKKPHKPKMKIGVSPPAKQLPGGRIFHSGYDNDPRGNLVYRFCVDKDE 300

Qy 301 TYDLLYQQCDAQPGAGSGYGVYVRMWKQQQKWERKIIGIPSGHQWYDMNGSPQDFNVAVR 360
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
301 TYDLLYQQCDAQPGAGSGYGVYVRMWKQQQKWERKIIGIPSGHQWYDMNGSPQDFNVAVR 360

Qy 361 ITPLKYAQICYWIKGNVLDREG 383
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
361 ITPLKYAQICYWIKGNVLDREG 383

Search completed: July 1, 2005, 21:32:16
Job time : 93.3582 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: July 1, 2005, 20:54:23 ; Search time 20.826 Seconds
(without alignments)
1811.048 Million cell updates/sec

Title: US-09-658-677-2

Perfect score: 2112

Sequence: 1 MAGIPGLFLRFLLCVAGQ.....IKGNLYDCREGDTVFLPGSN 392

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: PIR1.*

2: PIR2.*

3: PIR3.*

4: PIR4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	185	8.8	316	2 A45134	endopeptidase (EC
2	130.5	6.2	313	2 A35122	metalloproteinase
3	125	5.9	482	1 EXRT	coagulation factor
4	124	5.9	218	2 E97915	choline binding pr
5	118	5.6	269	2 B26823	pancreatic elastas
6	114	5.4	258	4 S70439	pancreatic elastas
7	114	5.4	267	4 A56615	probable pancreati
8	114	5.4	488	1 EXHU	coagulation factor
9	114	5.4	492	1 EXBO	coagulation factor
10	113	5.4	269	2 A26823	pancreatic elastas
11	113	5.4	271	2 A25528	pancreatic elastas
12	112.5	5.3	259	1 TRSGM	trypsin (EC 3.4.21
13	112	5.3	266	1 ELPG	pancreatic elastas
14	112	5.3	266	1 ELRT1	pancreatic elastas
15	112	5.3	522	2 TR2767	hypothetical prote
16	111.5	5.3	238	1 TRW5Y	trypsin-like prote
17	111.5	5.3	686	1 A59271	Ra-reactive factor
18	111	5.3	246	1 DBHU	complement factor
19	110	5.2	269	2 C26823	pancreatic elastas
20	109	5.2	761	2 JC5759	brain-specific ser
21	107.5	5.1	285	2 C95045	choline binding pr
22	107.5	5.1	405	2 T35117	probable secreted
23	106	5.0	236	2 A28566	T-cell suppressor
24	106	5.0	271	1 ELRT2	pancreatic elastas
25	104.5	4.9	273	2 E85765	hypothetical prote
26	104.5	4.9	273	2 H64915	putative protease
27	104.5	4.9	1582	2 T15308	hypothetical prote
28	102.5	4.9	2055	2 T31617	hypothetical prote
29	102	4.8	786	1 A47547	serine proteinase

30	101.5	4.8	278	2 AH0282	probable pepetidas
31	101.5	4.8	583	2 A29154	complement factor
32	101.5	4.8	747	2 I51579	complement factor
33	101	4.8	1047	2 A55617	masquerade precurs
34	99	4.7	274	2 S40004	trypsin-related pr
35	97.5	4.6	259	2 S68424	allergen Der f III
36	97.5	4.6	272	2 JC4170	trypsin-like prote
37	96	4.5	407	1 KFB07	coagulation factor
38	94.5	4.5	409	2 T35118	probable secreted
39	94.5	4.5	416	1 KFB0	coagulation factor
40	94.5	4.5	1238	2 T34929	hypothetical prote
41	94.5	4.5	2145	2 JC4747	adenylate cyclase
42	94	4.5	266	2 JC4850	trypsin-like prote
43	94	4.5	624	2 T02289	probable polygalac
44	94	4.5	855	2 JC7731	membrane-bound arg
45	93.5	4.4	452	1 A30351	coagulation factor

ALIGNMENTS

RESULT 1

A45134
endopeptidase (EC 3.4.-.-), glutamate-specific - Bacillus licheniformis
C:Species: Bacillus licheniformis
C>Date: 10-Jun-1993 #sequence_revision 18-Nov-1994 #text_change 16-Aug-2004
C/Accession: A45134; S23078
R:Kakudo, S.; Kikuchi, N.; Kitadokoro, K.; Fujiwara, T.; Nakamura, E.; Okamoto, H.; Shin, J. Biol. Chem. 267, 23782-23788, 1992
A>Title: Purification, characterization, cloning, and expression of a glutamic acid-speci
A/Reference number: A45134; MUID:93054737; PMID:1429718
A/Accession: A45134
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-316 <XAK>
A/Cross-references: UNIPROT:P80057; GB:D10060; NID:G216263; PIDN:BAA00949.1; PID:D100141;
A/Experimental source: ATCC 14580
A/Note: sequence extracted from NCBI backbone (NCBIN:118784, NCBIP:118785)
R:Svensden, I.; Breddam, K.
Eur. J. Biochem. 204, 165-171, 1992
A>Title: Isolation and amino acid sequence of a glutamic acid specific endopeptidase from
A/Reference number: S23078; MUID:92155199; PMID:1346764
A/Accession: S23078
A/Status: preliminary
A/Molecule type: protein
A/Residues: 95-316 <SVS>
C:Superfamily: Glutamyl endopeptidase, V8 type
C/Keywords: hydrolase

Query Match 8.8%; Score 185; DB 2; Length 316;

Best Local Similarity 23.2%; Pred. No. 4.2e-08;

Matches 77; Conservative 46; Mismatches 139; Indels 70; Gaps 16;

QY	63	SSGQCHKGTP	---PTVKEAKQVLSYETLYANGSRTEKXQVCIYLSGSGDAXXRDSG	119
DB	28	AQAAPSPH	---TPVSSDPSYK-AETSYVDP-----NIKSDQGLYSKAFITG---KVN	76
QY	120	SSGSKRRK	-----ROIYGYDSRFSIFGKDFLNPFPSTSVKLST---GCTGLVAE	167
DB	77	TKEAEKSPAK	APYSIKSVIGSDRTRVN---TTAYPYRAIVHSSIGSGCTGMIGP	133
QY	168	XHVLTAAHC	IHGKGT-YVKGTKLRVGLFKPKDGGGRANDSTAMPQMKFQWIRVKR	226
DB	134	KTVATAGHC	ITYDTSSGSPAGTATVSPG-----RNGTS-----YPYGSVKSTR	175
QY	227	THVPKGI	KNANDIGMDYDALLBLKPKHKFKMKIYVSPPAKQLPGCRIHPSGYDNR	286
DB	176	YFIPSGWR	SGNTN-----YDYGAIELSEFIGNTVGYGYSYTTSSLVGTTVITISGPGK	230
QY	287	PGNLVVR	FRCD---VKDETVDLLYQQCDAQPGASGYVYVRMKRQOQKWERKII---GIF	340
DB	231	TAGTQW	QHSGPTAISETYKLOYAM-DTYGGQSGSPVFEQSSSRSTNCSGCSLAVHTNGVY	289

QY 341 SGHWDVMSQPDNFVAVRITPLKVAQICYW 372
 Db 290 GG-----SSYNRGTRITTEVFNDLTNW 311

RESULT 2

A35122
 metalloprotease (EC 3.4.21.6) mpr precursor, extracellular - Bacillus subtilis
 C:Species: Bacillus subtilis
 C>Date: 27-Jul-1990 #sequence revision 27-Jul-1990 #text_change 16-Aug-2004
 C/Accession: A35122; I40010; A69660
 R:Sloma, A.; Rudolph, C.F.; Rufo Jr., G.A.; Sullivan, B.J.; Theriault, K.A.; Ally, D.; J. Bacteriol. 172, 1024-1029, 1990
 A>Title: Gene encoding a novel extracellular metalloprotease in Bacillus subtilis.
 A/Reference number: A35122; MUID:90130256; PMID:2105291
 A/Accession: A35122
 A/Status: preliminary
 A/Molecule type: DNA
 A/Residues: 1-313 <SLO>
 A/Cross-references: UNIPROT:P39790; GB:L10505; NID:g143209; PIDN:AAA22604.1; PID:g143210
 R:Smith, H.; de Jong, A.; Bron, S.; Venema, G.
 Gene 70, 351-361, 1988
 A>Title: Characterization of signal-sequence-coding regions selected from the Bacillus subtilis
 A/Reference number: I39994; MUID:89108019; PMID:3145906
 A/Accession: I40010
 A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: DNA
 A/Residues: 1-60, 65, 'L', 67, 'S', 69, 'AQA' <RES>
 A/Cross-references: GB:M22916; NID:g143701; PIDN:AAA22832.1; PID:g143702
 R:Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berte
 C.; Bron, S.; Brouillet, S.; Bruch, C.V.; Caldwell, B.; Capuano, J.; Carter, N.M.; Ch
 A.; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.
 Nature 390, 249-256, 1997
 A/Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Gall
 iech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F.
 Koetter, P.; Konigstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois,
 Y, M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelle
 Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanlon,
 A/Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Seron
 akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiyama
 T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yamamoto, K.; Yata, K.; Yoshida, K
 A/Authors: Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A.
 A>Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.
 A/Reference number: A69580; MUID:98044033; PMID:93384377
 A/Accession: A69660
 A/Status: preliminary; nucleic acid sequence not shown; translation not shown
 A/Molecule type: DNA
 A/Residues: 1-313 <KUN>
 A/Cross-references: GB:Z99105; GB:AL009126; NID:g2632457; PIDN:CAB12018.1; PID:el182176
 A/Experimental source: strain 168
 C/Genetics:
 A/Gene: mpr
 C/Superfamily: Glutamyl endopeptidase, V8 type
 C/Keywords: hydrolase

Query Match 6.2%; Score 130.5; DB 2; Length 313;
 Best Local Similarity 22.6%; Pred. No. 0.0018;
 Matches 87; Conservative 38; Mismatches 139; Indels 121; Gaps 19;

QY 28 WKETWPAFLPVVLPSTLNLAKPDFGAERAKLEVS-----SSCGPOCHKGTPLPTVYKEAK 82
 Db 7 FRKQWFAFLTVLCLALA---AAVSFGVPAKAENPQTSVNSGTKEA-DATKNQTSKADQ 61
 QY 83 QYLSYE-----TLVANGSRTEQVGIYTLSSGDGAXXRDSGSGSRKRRKQIYGYDS 135
 Db 62 VSAPIEGTGKTSKSLY--GGQTELEKNIOQLPS-----SIIGTDE 100
 QY 136 RFSIFGKDFLLNPPFSTSVKLSL-----CCTGTLVAEXHVLTAACHIH----- 178
 Db 101 RTRI-----SSSTSPFPRATVQLSIKYPNTSSTYCTGFLNPNVTVTAGHCVYSQDHGWS 157
 QY 179 -----DGKTVVKGTQKLRVGLPKPKFDGGRGANDSTSAMPEQKFWIRVKRTHVP 230

Db 158 TITAPGRNGSSYPYGT-----SGTMFYSVK-GWTESKDTNYD 195
 QY 231 KGWIKGN---ANDIGMDYDIALLELKPKHKKFMKIGVSPPAKQLPGGRHFSGYDNDRP 287
 Db 196 YCAIKLNGSPGNTVGM-YGYRTTNSSP-----VGLSSSVTGPCKDTFGTMSDTRP 247
 QY 288 GNLVRFCDKDETDYLLYQQCDAQFGASGYGVYVMKQKQKWERKIIGIFSGHQWVD 347
 Db 248 IR-----SAETVKLTLY-TTDTYGCQSGSPVY-----RNYSDTGQTAIAIHT----- 287
 QY 348 MNGSQPDNFVAVRITPLKVAQICYW 372
 Db 288 -NGG-SSYNLGRTRVNDVFNFIQYW 310
 RESULT 3
 EXPT
 coagulation factor Xa (EC 3.4.21.6) precursor - rat
 C:Species: Rattus norvegicus (Norway rat)
 C>Date: 31-Jan-1995 #sequence revision 07-Feb-1997 #text_change 09-Jul-2004
 C/Accession: S49075; Jc4670; PS0191; PS0190; I62745
 R:Stanton, C.; Ross, P.; Hutson, S.; Wallin, R.
 Thromb. Res. 80, 63-73, 1995
 A>Title: Evidence for competition between vitamin K-dependent clotting factors for intrac
 A/Reference number: A58498; MUID:96093366; PMID:8578539
 A/Accession: S49075
 A/Molecule type: mRNA
 A/Residues: 1-482 <STA>
 A/Cross-references: UNIPROT:Q63207; EMBL:X79807; NID:g506600; PIDN:CAA56202.1; PID:g50660
 A/Note: submitted to the EMBL Data Library, June 1994
 A/Note: neither the complete nucleic acid sequence nor the complete translation are show
 R:Stanton, C.; Ross, R.P.; Hutson, S.; Wallin, R.
 Gene 169, 269-273, 1996
 A>Title: Processing and expression of rat and human clotting factor-X-encoding cDNAs.
 A/Reference number: Jc4670; MUID:96194815; PMID:8647460
 A/Accession: Jc4670
 A/Molecule type: mRNA
 A/Residues: 1-482 <STA2>
 A/Cross-references: EMBL:X79807; NID:g506600; PIDN:CAA56202.1; PID:g506601
 A/Experimental source: Cos-1 cell
 R:Enjyoji, K.; Miyazaki, K.; Kato, H.
 J. Biochem. 109, 890-898, 1991
 A>Title: Characterization of rat factors X and Xa: demonstration of factor Xa in rat plas
 A/Reference number: PS0190; MUID:92041742; PMID:1718949
 A/Accession: PS0191
 A/Molecule type: protein
 A/Residues: 41-58, 'X', 60-65 <ENJ1>
 A/Accession: PS0190
 A/Molecule type: protein
 A/Residues: 183-186, 'X', 188-207 <ENJ2>
 R:Murakawa, M.; Okamura, T.; Kamura, T.; Kuroiwa, M.; Harada, M.; Niho, Y.
 Eur. J. Haematol. 52, 162-168, 1994
 A>Title: Analysis of the partial nucleotide sequences and deduced primary structures of .
 A/Reference number: I46196; MUID:94222160; PMID:8168596
 A/Accession: I62745
 A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: DNA
 A/Residues: 295-383, 'G', 385-455 <MUR>
 A/Cross-references: GB:D21215; NID:9415309; PIDN:BA04756.1; PID:g455396
 C/Function:
 A/Description: catalyzes the proteolytic activation of prothrombin to thrombin in the pre
 A/Pathway: blood coagulation
 C/Superfamily: coagulation factor X; EGF homology; Gla domain homology; tryptsin homology
 C/Keywords: beta-hydroxyaspartic acid; blood coagulation; calcium binding; carboxylglutami
 F:1-23/Domain: signal sequence #status predicted <SIG>
 F:24-40/Domain: propeptide #status predicted <PRO>
 F:41-179/Product: coagulation factor X light chain #status predicted <LCH>
 F:129-164/Domain: EGF homology <EG1>
 F:183-482/Product: coagulation factor X heavy chain #status predicted <HCH>
 F:183-231/Domain: activation peptide #status predicted <APT>

[illegible]

Eur. J. Biochem. 218, 153-163, 1993
A:Title: Identification of O-linked oligosaccharide chains in the activation peptides of
A:Reference number: S39414; MUID:94062825; PMID:8243461
A:Accession: S39415
A:Molecule type: protein
A:Residues: 183-234 <INO>
A:Note: glycosylation sites
R:Jagadeeswaran, P.; Reddy, S.V.; Rao, K.J.; Hamsabhuhanam, K.; Lyman, G.
Gene 84, 517-519, 1989
A:Title: Cloning and characterization of the 5' end (exon 1) of the gene encoding human
A:Reference number: I54051; MUID:90128299; PMID:2612918
A:Accession: I54051
A:Status: translation not shown; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-23 <RES>
A:Cross-references: GB:M33297; NID:g183860; PIDN:AA52636.1; PID:g553330
R:Padmanabhan, K.; Padmanabhan, K.P.; Tulinsky, A.; Park, C.H.; Bode, W.; Huber, R.; Bla
J. Mol. Biol. 232, 947-966, 1993
A:Title: Structure of human des(1-45) factor Xa at 2.2 angstroms resolution.
A:Reference number: A49458; MUID:93360277; PMID:8355279
A:Contents: annotation; X-ray crystallography, 2.2 angstroms
C:Comment: The two chains held together by one disulfide bond are formed from a single-c
C:Comment: The activation peptide is cleaved by factor IXa (in the intrinsic pathway) or
C:Genetics:
A:Gene: GDB:F10
A:Cross-references: GDB:119890; OMIM:227600
A:Map position: 13q34-13q34
A:Introns: 24/1; 77/3; 86/1; 124/1; 150/3; 249/3; 289/1
A:Note: deficiency of this factor causes Stuart disease
C:Function:
A:Description: catalyzes the proteolytic activation of prothrombin to thrombin in the pr
A:Pathway: blood coagulation
C:Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homology
C:Keywords: beta-hydroxyaspartic acid; blood coagulation; calcium binding; carboxyglutam
F:1-23/Domain: signal sequence #status predicted <SIG>
F:24-40/Domain: propeptide #status predicted <PRO>
F:25-84/Domain: Gla domain homology <GLA>
F:41-179/Product: coagulation factor X light chain #status experimental <LCH>
F:90-121/Domain: EGF homology <EG1>
F:129-164/Domain: EGF homology <EG2>
F:183-488/Product: coagulation factor X heavy chain #status experimental <HCH>
F:183-234/Domain: activation peptide #status experimental <APT>
F:235-488/Product: coagulation factor Xa heavy chain #status experimental <ACT>
F:235-462/Domain: trypsin homology <TRY>
F:46,47,54,56,59,60,65,66,69,72,79/Modified site: gamma-carboxyglutamic acid (Glu) #stat
F:57-62/Disulfide bonds: #status predicted
F:90-101,95-110,112-121,129-140,136-149,151-164,172-342,241-246,261-277,390-404,415-443/
F:103/Modified site: erythro-beta-hydroxyaspartic acid (Asp) #status experimental
F:199,211/Binding site: carboxylate (Thr) (covalent) #status experimental
F:221,231/Binding site: carboxylate (Asn) (covalent) #status experimental
F:234-235/Cleavage site: Arg-Ile (coagulation factor IXa, coagulation factor VIIa) #stat
F:276,322,419/Active site: His, Asp, Ser #status experimental

Query Match 5.4%; Score 114; DB 1; Length 488;
Best Local Similarity 20.9%; Pred. No. 0.08;
Matches 57; Conservative 37; Mismatches 67; Indels 112; Gaps 13;
QY 160 CTGTLVAEXHLVTAACHIDHDKTYVKGTKLVGFLKPKFGCGRGANDSTAMPQMKF 219
DB 261 CGGTILSEFILTANCLVQAKF-----KVRVGRDNTQEEGEAVHE-VEVVIKHNFP 314
QY 220 QWIRVTRTHVPKGIWKNANDIGMDYDYLLELLKPKRKMIGVSPPA----- 269
DB 315 -----TKETV-----DFDIIVLRKLTPTIT---FRMNVAPACLPDRDAEST 352
QY 270 --KQLPG-----CRIHFGVDNDPRGNLVYRFDVKD-----ETYDLLVQ 307
DB 353 LMTQTKTGVSGFGRTEKGRQSTRLKMLKEVPYVYDRNSCKLSSSFIITQNMFCAGYDT--K 410
QY 308 QCDAPQPCASG-----YGVYVRMKRQKQKWERKIIGI 339
DB 411 QEDACQDGGPHTVRFKDTYFTVIGVSGEGCARKGKGIYTK-----V 455

QY 340 FSGHQWDMN-----GSPQDFNVAVRI---TPLK 365
DB 456 TAPLKWIDRSMKTRGLPKAKSHAPEVITSSPLK 488
RESULT 9
EXPO
coagulation factor Xa (EC 3.4.21.6) precursor - bovine
N:Alternate names: Stuart factor
C:Species: Bos primigenius taurus (cattle)
C:Date: 24-Apr-1984 #sequence revision 17-Mar-1987 #text change 09-Jul-2004
C:Accession: A22867; A14997; A12030; A34412; S39414; A00925
R:Pung, M.R.; Campbell, R.M.; MacGillivray, T.A.
Nucleic Acids Res. 12, 4481-4492, 1984
A:Title: Blood coagulation factor X mRNA encodes a single polypeptide chain containing a
A:Reference number: A22867; MUID:84247315; PMID:6330671
A:Accession: A22867
A:Molecule type: mRNA
A:Residues: 1-487 <FUN>
A:Cross-references: UNIPROT:P00743; GB:X00673; NID:g192; PIDN:CAA25286.1; PID:g193
R:Enfield, D.L.; Ericsson, L.H.; Fujikawa, K.; Walsh, K.A.; Neurath, H.; Titani, K.
Biochemistry 19, 659-667, 1980
A:Title: Amino acid sequence of the light chain of bovine factor X-1 (Stuart factor).
A:Reference number: A14997; MUID:80130563; PMID:6766735
A:Accession: A14997
A:Molecule type: protein
A:Residues: 41-102, 'N', 104-180 <ENF>
R:McMullen, B.A.; Fujikawa, K.; Kisiel, W.
Biochem. Biophys. Res. Commun. 115, 8-14, 1983
A:Title: The occurrence of beta-hydroxyaspartic acid in the vitamin K-dependent blood co
A:Reference number: A20274; MUID:83308813; PMID:6688526
A:Contents: annotation; revision to residue 103
R:Titani, K.; Fujikawa, K.; Enfield, D.L.; Ericsson, L.H.; Walsh, K.A.; Neurath, H.
Proc. Natl. Acad. Sci. U.S.A. 72, 3082-3086, 1975
A:Title: Bovine factor X-1 (Stuart factor): amino-acid sequence of heavy chain.
A:Reference number: A12030; MUID:76053069; PMID:1059093
A:Accession: A12030
A:Molecule type: protein
A:Residues: 183-292,294-295, 'GDE', 299-334,336-348, 'AB', 351-354,356-441, 'GKFG', 446-492 <TJ
A:Note: carboxylate binding sites and disulfide bonds were determined
R:Persson, E.; Selander, M.; Linse, S.; Drakenberg, T.; Oehlin, A.K.; Stenflo, J.
J. Biol. Chem. 264, 16897-16904, 1989
A:Title: Calcium binding to the isolated beta-hydroxyaspartic acid-containing epidermal s
A:Reference number: A34412; MUID:89380326; PMID:2789221
A:Accession: A34412
A:Molecule type: protein
A:Residues: 85-126 <PER>
A:Note: beta-hydroxyaspartic acid site
R:Inoue, K.; Morita, T.
Eur. J. Biochem. 218, 153-163, 1993
A:Title: Identification of O-linked oligosaccharide chains in the activation peptides of
A:Reference number: S39414; MUID:94062825; PMID:8243461
A:Accession: S39414
A:Molecule type: protein
A:Residues: 183-196;199-209;216-233 <INO>
A:Note: carboxylate binding sites
R:Titani, K.; Hermanson, M.A.; Fujikawa, K.; Ericsson, L.H.; Walsh, K.A.; Neurath, H.; Dr
Biochemistry 11, 4899-4903, 1972
A:Title: Bovine factor X-la (activated Stuart factor). Evidence of homology with mammali
A:Reference number: A12453; MUID:73053314; PMID:4264286
A:Contents: annotation; active site
R:Fujikawa, K.; Titani, K.; Davie, E.W.
Proc. Natl. Acad. Sci. U.S.A. 72, 3359-3363, 1975
A:Title: Activation of bovine factor X (Stuart factor): conversion of factor Xaalpha to i
A:Reference number: A13504; MUID:76053121; PMID:1059122
A:Contents: annotation; activation
R:Sugo, T.; Bjork, I.; Holmgren, A.; Stenflo, J.
J. Biol. Chem. 259, 5705-5710, 1984
A:Title: Calcium-binding properties of bovine factor X lacking the gamma-carboxyglutamic
A:Reference number: A38024; MUID:84185716; PMID:6546930
A:Contents: annotation; calcium binding
R:Morita, T.; Jackson, C.M.

A;Accession: A26823
A;Molecule type: mRNA
A;Residues: 1-269 <KAW>
A;Cross-references: UNIPROT:P08419; GB:M16651; NID:gl64441; PIDN:AAA31027.1; PID:gl64442
C;Superfamily: trypsin; trypsin homology
C;Keywords: hydrolase; serine proteinase
F;1-16/Domain: signal sequence #status predicted <SIG>
F;17-28/Domain: propeptide #status predicted <PRO>
F;29-269/Product: elastase II #status predicted <MAT>
F;29-262/Domain: trypsin homology <TRY>
F;73,121,216/Active site: His, Asp, Ser #status predicted

Query Match 5.4%; Score 113; DB 2; Length 269;
Best Local Similarity 27.1%; Pred. No. 0.048;
Matches 59; Conservative 28; Mismatches 65; Indels 66; Gaps 14;

QY 128 ROIYGVDSRFSFGDKFLNYPFSTSVKL-STG-----CTGLVAEXHVLTAACHIDCK 181
| | | | | : | | : | | : | | | | | : | | | | | :
Db 28 RVVGEDARPN-----SWPQVSLQVDSGQWRHTCGGTLVDQSWVLTAAHCISSR 79
| | | | | : | | : | | : | | | | | : | | | | | :
QY 182 TY--VKGTQKLRVGLPKPKFGDGRGANDSTAMPEQMKFQIRVKRTHVPKGIWKGNAN 239
| | | | | : | | : | | : | | | | | : | | | | | :
Db 80 TRRVVLGRHSL-----STNEPGSLA-----VKSKLVVHQDW---NSN 114
| | | | | : | | : | | : | | | | | : | | | | | :
QY 240 DIGMDYDVALLELKKP-HKRKPMKIGVSPPAKQ-LPG-----GRHFSGYDND--R 286
| | | | | : | | : | | : | | | | | : | | | | | :
Db 115 QLSNGNDIALKLASPSVLTDKIQLGCLPAAGTILPNNVVCYVTGWGRLQTNAGSPDILQ 174
| | | | | : | | : | | : | | | | | : | | | | | :
QY 287 PGNLYVRFCQVDKTYDILLYQOCDAPQAGSGYGVVRM 324
| | | | | : | | : | | : | | | | | : | | | | | :
Db 175 OGQLL-----VVD-----YATC-SKPGMWGSTVKTNM 200
| | | | | : | | : | | : | | | | | : | | | | | :

RESULT 11
A25528
A;Title: Sequence organisation and transcriptional regulation of the mouse elastase II
A;Reference number: A93646; MUID:87066713; PMID:3641189
A;Accession: A25528
A;Molecule type: mRNA
A;Residues: 1-271 <STE>
A;Cross-references: UNIPROT:P05208; GB:X04573; NID:G50825; PIDN:CAA28242.1; PID:G50826
C;Superfamily: trypsin; trypsin homology
C;Keywords: hydrolase; serine proteinase
F;1-30/Domain: signal sequence #status predicted <SIG>
F;31-271/Product: pancreatic elastase II #status predicted <MAT>
F;31-264/Domain: trypsin homology <TRY>
F;75,123,218/Active site: His, Asp, Ser #status predicted

Query Match 5.4%; Score 113; DB 2; Length 271;
Best Local Similarity 29.0%; Pred. No. 0.048;
Matches 38; Conservative 22; Mismatches 37; Indels 34; Gaps 7;

QY 148 YPFSTSVK-LSTG-----CTGLVAEXHVLTAACHIDGKTY--VKGTQKLRVGLPKPKF 199
| | | | | : | | : | | : | | | | | : | | | | | :
Db 42 WPMQVSLQVLSGRVRHNCGSLVANNWVLTAAHCLSNVQTYRVLLGAHSL----- 92
| | | | | : | | : | | : | | | | | : | | | | | :
QY 200 KDGGRGANDSTAMPEQMKFQIRVKRTHVPKGIWKGNANDIGMDYDVALLELKKP-HKR 258
| | | | | : | | : | | : | | | | | : | | | | | :
Db 93 --SNPFGASAA-----VQVSKLVVHQRW---NSQNVNGYDIALIKLASPVTLS 136
| | | | | : | | : | | : | | | | | : | | | | | :
QY 259 KPMKIGVSPPA 269
| | | | | : | | : | | : | | | | | : | | | | | :
Db 137 KNIQIACLPAA 147
| | | | | : | | : | | : | | | | | : | | | | | :

RESULT 12
TRSMG

trypsin (EC 3.4.21.4) precursor - Streptomyces griseus
C:Species: Streptomyces griseus
C>Date: 24-Apr-1984 #sequence_revision 12-May-1994 #text_change 09-Jul-2004
C:Accession: JQ1302; A00962
R:Kim, J.C.; Cha, S.H.; Jeong, S.T.; Oh, S.K.; Byun, S.M.
Biochem. Biophys. Res. Commun. 181, 707-713, 1991
A:Title: Molecular cloning and nucleotide sequence of Streptomyces griseus trypsin gene.
A:Reference number: JQ1302; MUID:92095977; PMID:1755852
A:Accession: JQ1302
A:Molecule type: DNA
A:Residues: 1-259 <XIM>
A:Cross-references: UNIPROT:P00775; GB:M64471
A:Experimental source: strain ATCC10137
R:Olafson, R.W.; Jurasek, L.; Carpenter, M.R.; Smillie, L.B.
Biochemistry 14, 1168-1177, 1975
A:Title: Amino acid sequence of Streptomyces griseus trypsin. Cyanogen bromide fragments
A:Reference number: A00962; MUID:75127940; PMID:804314
A:Accession: A00962
A:Molecule type: protein
A:Residues: 37-95,98-259 <OLA>
R:Read, R.J.; James, M.N.G.
J. Mol. Biol. 200, 523, 1988
A:Title: Refined crystal structure of Streptomyces griseus trypsin at 1.7 angstroms resolution
A:Reference number: A44574; MUID:88286735; PMID:3135412
A:Contents: annotation; X-ray crystallography, 1.7 angstroms
A>Note: residues 96-97 modeled as Gly-Ala
C:Genetics:
A:Gene: sprt
C:Superfamily: trypsin; trypsin homology
C:Keywords: hydrolase; serine proteinase
F:1-32/Domain: signal sequence #status predicted <SIG>
F:33-36/Domain: propeptide #status predicted <PRO>
F:37-258/Product: trypsin #status experimental <MAT>
F:37-252/Domain: trypsin homology <TRY>
F:58-74,177-192,204-233/Disulfide bonds: #status experimental
F:73,118,208/Active site: His, Asp, Ser #status experimental
Query Match 5.3%; Score 112.5; DB 1; Length 259;
Best Local Similarity 26.0%; Pred. No. 0.05;
Matches 39; Conservative 21; Mismatches 53; Indels 37; Gaps 5;
QY 148 YPFSTSVKLSGCTGLVAEXHVLTAACHTIDGKTVKQKLVGFLKPKFKDGGGAN 207
DB 48 FPF--WVRLSMGCGGALYQAQDIVLTAACHV-----SSGNN 81
QY 208 DS---TSANPEQMKFQWIRKTHVPKGIKGNANDIGMDYDVALLELKKPKFKMKTG 264
DB 82 TSITATGGVVDLQSSSAVKVRSTKVLQA-----PGYNGTGKDWALFKLAQPINQPTLKIA 136
QY 265 VSPPAKQLPGRIHFGSYNDNRGNLYVRF 294
DB 137 TTTAYNQ---GTTTAVAGWGANREGGQQRY 163
RESULT 13
ELPG
pancreatic elastase (EC 3.4.21.36) I precursor - pig
C:Species: Sus scrofa domestica (domestic pig)
C>Date: 24-Apr-1984 #sequence_revision 30-Sep-1990 #text_change 09-Jul-2004
C:Accession: JS0013; A26777; A10061; A00959
R:Shirau, Y.; Yoshida, H.; Mikayama, T.; Matsuki, S.; Tanaka, J.I.; Ikenaga, H.
J. Biochem. 99, 1707-1712, 1986
A:Title: Isolation and expression in Escherichia coli of a cDNA clone encoding porcine H
A:Reference number: A92005; MUID:86304235; PMID:3528137
A:Accession: JS0013
A:Molecule type: mRNA
A:Residues: 1-266 <SHI>
A:Cross-references: UNIPROT:P00772; GB:X04036; GB:D00070; GB:N00070; NID:91941; PIDN:CAA
R:Fan, T.; Kawashima, I.; Furukawa, H.; Ohmine, T.; Takiguchi, Y.
J. Biochem. 101, 591-599, 1987
A:Title: Characterization of a silent gene for human pancreatic elastase I: structure of
A:Reference number: A26777; MUID:87250343; PMID:3648024
A:Accession: A26777

A:Molecule type: mRNA
A:Residues: 1-125,'G', 127-183,'L', 185-266 <TAN>
A:Cross-references: GB:D00160; NID:9217683; PIDN:BAA00118.1; PID:9217684
A>Note: the authors translated the codon GGG for residue 58 as Gln, GGC for residue 126 &
R:Shotton, D.M.; Hartley, B.S.
Biochem. J. 131, 643-675, 1973
A:Title: Evidence for the amino acid sequence of porcine pancreatic elastase.
A:Reference number: A90267; MUID:73229121; PMID:4578945
A:Accession: A10061
A:Molecule type: protein
A:Residues: 27-91,'N', 93-203,'N', 205-266 <SHO>
R:Shotton, D.M.; Hartley, B.S.
Nature 225, 811-816, 1970
A:Title: Three-dimensional structure of tosyl-elastase.
A:Reference number: A93160; MUID:70114044; PMID:5415110
A:Contents: annotation; X-ray crystallography, 3.5 angstroms; active site
C:Superfamily: trypsin; trypsin homology
C:Keywords: hydrolase; pancreas; serine proteinase; zymogen
F:1-16/Domain: signal sequence #status predicted <SIG>
F:17-26/Domain: activation peptide #status predicted <APT>
F:27-266/Product: elastase I #status experimental <MAT>
F:27-259/Domain: trypsin homology <TRY>
F:56-72,153-220,184-200,210-240/Disulfide bonds: #status experimental
F:71,119,214/Active site: His, Asp, Ser #status experimental
Query Match 5.3%; Score 112; DB 1; Length 266;
Best Local Similarity 27.3%; Pred. No. 0.057;
Matches 36; Conservative 21; Mismatches 41; Indels 34; Gaps 6;
QY 147 NYPFSTSVKLSG-----CTGTLVAEXHVLTAACHTIDGKTV--VKGTQKLVGFLKPK 198
DB 37 SWPSQISLQYRSGSSWAHTCGGTLIRQNWVMTAAHCVDELFRVVVGHNL----- 88
QY 199 FKDGGRGANDSTSAMPEQMKFQWIRKTHVPKGIKGNANDIGMDYDVALLEL-KKPKH 257
DB 89 -----NQNDGTE-----QYVGQKIVVHPYV---NTDDVAAGYDIALRLAQSVTL 131
QY 258 RKFMKIGVSPPA 269
DB 132 NSYVQLGVLPRA 143
RESULT 14
ELRT1
pancreatic elastase (EC 3.4.21.36) I precursor - rat
C:Species: Rattus norvegicus (Norway rat)
C>Date: 18-Aug-1982 #sequence_revision 18-Aug-1982 #text_change 09-Jul-2004
C:Accession: A00960; A20534
R:MacDonald, R.J.; Swift, G.H.; Quinto, C.; Swain, W.; Pictet, R.L.; Nikovits, W.; Rutten
Biochemistry 21, 1453-1463, 1982
A:Title: Primary structure of two distinct rat pancreatic preproelastases determined by
A:Reference number: A00960; MUID:82182967; PMID:6918221
A:Accession: A00960
A:Molecule type: mRNA
A:Residues: 1-266 <MAC>
A:Cross-references: UNIPROT:P00773; GB:V01234; NID:956088; PIDN:CAA24544.1; PID:956089
R:Largman, C.
Biochemistry 22, 3763-3770, 1983
A:Title: Isolation and characterization of rat pancreatic elastase.
A:Reference number: A20534; MUID:84000385; PMID:6555050
A:Accession: A20534
A:Molecule type: protein
A:Residues: 17-37,'X', 39-45 <LAR>
C:Superfamily: trypsin; trypsin homology
C:Keywords: hydrolase; pancreas; serine proteinase; zymogen
F:1-16/Domain: signal sequence #status predicted <SIG>
F:17-26/Domain: activation peptide #status predicted <APT>
F:27-266/Product: elastase I #status predicted <MPT>
F:27-259/Domain: trypsin homology <TRY>
F:71,119,214/Active site: His, Asp, Ser #status predicted
Query Match 5.3%; Score 112; DB 1; Length 266;
Best Local Similarity 26.7%; Pred. No. 0.057;

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 1, 2005, 20:53:37 ; Search time 92.7095 Seconds
(without alignments)
2165.204 Million cell updates/sec

Title: US-09-658-677-2

Perfect score: 2112

Sequence: 1 MAGIGLFLFLFLCAVQ.....IKGNVLDRCRGDTVFLPGSN 392

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt 03:*

1: uniprot_sprot:*

2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2044	96.8	383	1 PS23 HUMAN	O95084 homo sapien
2	1881	89.1	383	2 O6AY61	O6ay61 rattus norv
3	1866.5	88.4	382	1 PS23 MOUSE	O9d6x6 mus musculu
4	1860.5	88.1	382	2 O8BZS4	O8bz84 mus musculu
5	1029	48.7	413	2 O9BQP6	O9bqp6 homo sapien
6	1028	48.7	413	2 O8N320	O8n320 homo sapien
7	1003.5	47.5	409	2 O8CQF9	O8cqf9 mus musculu
8	998.5	47.3	409	2 O8CQ15	O8cq15 mus musculu
9	994.5	47.1	418	2 O6GML6	O6gm16 brachydanio
10	992.5	47.0	409	2 O8CQD6	O8cq06 mus musculu
11	185	8.8	316	1 GSEP BACLI	P80057 bacillus li
12	185	8.8	316	2 O65NR6	O65nr6 bacillus li
13	182	8.6	450	2 O71YE5	O71ye5 listeria mo
14	165.5	7.8	364	2 O98G17	O98g17 rhizobium i
15	156	7.4	271	2 O987W6	O987w6 rhizobium i
16	133.5	6.3	358	2 O931E7	O931e7 staphylococ
17	132.5	6.3	323	2 O73DS4	O73ds4 bacillus ce
18	132	6.2	267	2 O6DGW4	O6dgw4 brachydanio
19	130.5	6.2	313	1 MPR BACSU	P39790 bacillus su
20	130	6.2	469	2 O9GMD9	O9gm9 ornithorhyn
21	129.5	6.1	321	2 O7NGB4	O7ngb4 gloeobacter
22	128.5	6.1	678	2 O9JJ58	O9jj58 rattus norv
23	128.5	6.1	1322	2 O9NAT0	O9nat0 anopheles g
24	128	6.1	266	2 O6AZC0	O6azc0 brachydanio
25	125.5	5.9	339	2 O9QX91	O9qx91 rattus norv
26	125.5	5.9	366	2 O9QX85	O9qx85 rattus norv
27	125.5	5.9	541	2 O9QX90	O9qx90 rattus norv
28	125.5	5.9	623	2 O9JJ73	O9jj73 rattus norv
29	125.5	5.9	643	2 O9QX84	O9qx84 rattus norv
30	125.5	5.9	1234	2 O7P1Q7	O7p1q7 anopheles g
31	125.5	5.9	1322	2 O7PNR7	O7pnr7 anopheles g

32	125.5	5.9	1322	2	O9NJS5	O9nj55 anopheles g
33	125	5.9	482	1	FA10 RAT	O63207 rattus norv
34	124.5	5.9	290	2	O81HL5	O81hl5 bacillus ce
35	124	5.9	218	2	O8DR41	O8dr41 streptococc
36	123.5	5.8	376	1	FA10 HOPST	P83370 hoptocephal
37	123	5.8	259	2	O9XY61	O9xy61 ctienocephal
38	123	5.8	266	2	O46644	O46644 macaca fasc
39	123	5.8	352	2	O6UWB4	O6uwb4 homo sapien
40	122.5	5.8	303	2	O9EXR9	O9exr9 bacillus in
41	122.5	5.8	490	1	FA10 RABIT	OL9045 oryctolagus
42	121	5.7	745	2	O9OMF9	O9omf9 triakis scy
43	120	5.7	269	2	O6ICV2	O6icv2 homo sapien
44	120	5.7	269	2	O6ISU5	O6isu5 homo sapien
45	120	5.7	685	2	O91WP0	O91wp0 mus musculu

ALIGNMENTS

RESULT 1
PS23_HUMAN STANDARD; PRT; 383 AA.
ID AC O95084;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Serine protease 23 precursor (EC 3.4.21.-) (Putative secreted protein
DE ZSIG13) (UNQ270/PRO307).
GN Name=PRSS23; Synonym=ZSIG13;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Umbilical vein;
RA Li X., Tedder T.F.;
RT "A novel serine protease from human umbilical vein endothelial
RT cells.";
RL Submitted (JUL-1997) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Sheppard P., Blumberg H., Jelinek L., Foster D., O'Hara P.;
RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Uterus;
RA Wiemann S., Weil B., Wellenreuther R., Gassenhuber J., Glaesl S.,
RA Ansoerge W., Boecker H., Bloeker H., Bauersachs S., Blum H.,
RA Lauber J., Dueterthof A., Beyer A., Koehrer K., Strack N.,
RA Mewes H.-W., Ottenwaelder B., Obermaier B., Tampe J., Heubner D.,
RA Wambutt R., Korn B., Klein M., Poustka A.;
RT "Towards a catalog of human genes and proteins: sequencing and
RT analysis of 500 novel complete protein coding human cDNAs.";
RL Genome Res. 11:422-435 (2001).
RN [4]
RP SEQUENCE FROM N.A.
RA Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D., Brueh J.,
RA Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,
RA Eaton D., Foster J., Grimaldi C., Gu Q., Hass P.E., Heldens S.,
RA Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,
RA Lewis L., Liao D., Mark M., Robbie E., Sanchez C., Schoenfeld J.,
RA Seshagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A.,
RA Vandlen R., Watanabe C., Wieand D., Woods K., Xie M.-H., Yaneura D.,
RA Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I.,
RA Godowski P., Gray A.;
RT "The secreted protein discovery initiative (SPDI), a large-scale
RT effort to identify novel human secreted and transmembrane proteins: a
RT bioinformatics assessment.";
RL Genome Res. 13:2265-2270 (2003).
RN [5]

DR InterPro; IPR001314; Peptidase SIA.
 DR InterPro; IPR009003; Pept Ser_Cys.
 DR Pfam; PF00089; Trypsin_1.
 DR PRINTS; PR00722; CHYMOTRYPSIN.
 DR ProDom; PD001827; Histone H4; 1.
 DR PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.
 KW Hydrolyase; Hypothetical protein; Protease; Serine protease.
 SQ SEQUENCE 383 AA; 43159 MW; 4AB13CC7B66CDP8 CRC64;

Query Match 89.18; Score 1881; DB 2; Length 383;
 Best Local Similarity 90.3%; Pred. No. 2.6e-158;
 Matches 346; Conservative 11; Mismatches 26; Indels 0; Gaps 0;

OY 1 MAGIPGLLFLFLLCAGVGSPVSPAPKPTWPAIRLPVVLPOSTLNLAKPDFGAEAKLE 60
 DB 1 MAGIPGLLILLVLLCVPMQSPVNPVWKTWPAIRLPVLPQSTLKLAPDFDAKLE 60

OY 61 VSSSCGQCHKGTPLPYKBAQYLSYETLYANGSRTEQVGIVYLSSGSGDGAAXRDSGS 120
 DB 61 VSSSCGQCHKGTPLPYKBAQYLSYETLYANGSRTEQVGIVYLSSGSGRARSRDEA 120

OY 121 SGKSRKQRIQYGVDSRISFGKDFLLNYPSTSVKLTGCTGTGLVAEKHVLTAACHIDG 180
 DB 121 AGKSRKQRIQYGVDSRISFGKDFLLNYPSTSVKLTGCTGTGLVAEKHVLTAACHIDG 180

OY 181 KTVYKGTQKLRVGLFKPKFGKGGRGANDSTSAPEQMKFQWIRKTRTHVPKGIKGNAND 240
 DB 181 KTVYKGTQKLRVGLFKPKFGKGGRGANDSTSAPEQMKFQWIRKTRTHVPKGIKGNAND 240

OY 241 IGMDDYDVALLELKKPKRKFPMKIGVSPPAQLPGRIHFSGYDNDPGRNLVYRFDVKDE 300
 DB 241 IGMDDYDVALLELKKPKRKFPMKIGVSPPAQLPGRIHFSGYDNDPGRNLVYRFDVKDE 300

OY 301 TYDLLVQCCDAQPGASGYGVYVWKRQKQKWKRIIGFSGHQWDMNGSPQDFNVAVR 360
 DB 301 TYDLLVQCCDAQPGASGYGVYVWKRQKQKWKRIIGFSGHQWDMNGSPQDFNVAVR 360

OY 361 ITPKVAQICYNKGNLYDCREG 383
 DB 361 ITPKVAQICYNKGNLYDCREG 383

RESULT 3

PS23_MOUSE STANDARD; PRT; 382 AA.

AC Q9D6X6; Q8VEG1;
 DT 28-FEB-2003 (Rel. 41, Last sequence)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 25-OCT-2004 (Rel. 45, Last annotation update)
 DE Serine protease 23 precursor (EC 3.4.21.-).
 GN Name=Pr8e23;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]

SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Tongue;
 RX MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
 RA Okazaki Y., Furuno M., Kaakawa T., Adachi J., Bono H., Kondo S.,
 RA Nikaido I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
 RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,
 RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
 RA Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
 RA Blake J.A., Bradt D., Brusci V., Chothia C., Corbani L.E., Cousins S.,
 RA Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,
 RA Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
 RA Grimmond S., Guetincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
 RA Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,
 RA Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
 RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
 RA Nagashima T., Numata K., Okido T., Pavan W.J., Perlea G., Pesole G.,
 RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,

RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
 RA Sandelin A., Schneider C., Sempile C.A., Setou M., Shimada K.,
 RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tonita M.,
 RA Verardo R., Wagner L., Wahlstedt C., Wang Y., Watanabe Y., Wells C.,
 RA Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L.,
 RA Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
 RA Hironaka-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
 RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
 RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
 RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shingawa A.,
 RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
 RA Birney E., Hayashizaki Y.;
 RT "Analysis of the mouse transcriptome based on functional annotation of
 RL 60,770 full-length cDNAs";
 RL Nature 420:563-573 (2002).
 RP SEQUENCE FROM N.A.
 RC TISSUE=Breast tumor;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Sherman C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haefl F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaney S.J.,
 RA Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Pahey J., Helton B., Kettaman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grooming J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RL and mouse cDNA sequences";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 CC -!- SUBCELLULAR LOCATION: Secreted (Potential).
 CC -!- SIMILARITY: Belongs to the peptidase S1 family.
 CC -----
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 CC -----
 DR EMBL; AK009847; BAB26541.1; -;
 DR EMBL; AK078518; BAC37319.1; -;
 DR EMBL; BC018517; AAH18517.1; -;
 DR HSSP; P00746; IDSU
 DR MEROPS; S01.309; -;
 DR MGI; 1923703; 2310046G15Rik.
 DR InterPro; IPR009003; Pept Ser_Cys.
 DR InterPro; IPR001254; Peptidase S1.
 DR InterPro; IPR001314; Peptidase_S1A.
 DR Pfam; PF00089; Trypsin; 1.
 DR PRINTS; PR00722; CHYMOTRYPSIN.
 DR SMART; SM00020; TRYP_SPC; 1.
 DR PROSITE; PS00240; TRYPSIN_DOM; FALSE_NEG.
 DR PROSITE; PS00134; TRYPSIN_HIS; 1.
 DR PROSITE; PS00135; TRYPSIN_SER; FALSE_NEG.
 KW Hydrolyase; Serine protease; Signal
 FT SIGNAL 1 22 Potential.
 FT CHAIN 23 382 Serine protease 23.
 FT ACT_SITE 174 174 Charge relay system (By similarity).
 FT ACT_SITE 239 239 Charge relay system (By similarity).
 FT ACT_SITE 315 315 Charge relay system (By similarity).
 FT DISULFID 159 175 By similarity.
 FT CARBOHYD 92 92 N-linked (GlcNAc...) (Potential).

FT	CARBOHYD	206	206	N-linked (GlcNAc...) (Potential).							
RC	CONFLICT	260	260	M -> I (in Ref. 1; BAB26541).							
SQ	SEQUENCE	382 AA;	43071 MW;	6F09A5C80A5B2306 CRC64;							
Query Match											
Best Local Similarity 88.4%; Score 1866.5; DB 1; Length 382;											
Matches 344; Conservative 14; Mismatches 24; Indels 1; Gaps 1;											
QY	1	MAGIPGLLFLFLLCAVGQVSPYAPWKPPTWPAVRLPVVLPQSTLNLAQDFGAEAKLE	60								
DB	1	MAGIPG-LFILLVLLCVFMQVSPYTPWKPPTWPAVRLPVVLPQSTLNLAQDFDAKLE	59								
QY	61	VSSSCGPGCHKTPLPTTYKEAQYLSYETLYANGSRTXQVGIYILSSSGDGAXXRDSGS	120								
DB	60	VSSSCGPGCHKTPLPTTYEAAQYLSYETLYANGSRTXQVGIYILSSSGDGAXXRDSGA	119								
QY	121	SGKSRKRIQYGYDSRFSIFGKDFLLNYPFSTSVKLSCTGCTGLVAEXHVLTAACHIDG	180								
DB	120	TGSRKRIQYGYDSRFSIFGKDFLLNYPFSTSVKLSCTGCTGLVAEXHVLTAACHIDG	179								
QY	181	KTYVKGTQKLRLVGLFKPKFQKGGRGANDSTSAMPEQMKFQIRVKTHTVPGWIKGNAND	240								
DB	180	KTYVKGTQKLRLVGLFKPKYKDGAGDNSSSSAMPDKMKFQIRVKTHTVPGWIKGNAND	239								
QY	241	IGMDYDVALLELKKPHKPKMKIGVSPPAKQLPGGRHFSGYDNDPRGNLVTRPCDVKDE	300								
DB	240	IGMDYDVALLELKKPHKPKMKIGVSPPAKQLPGGRHFSGYDNDPRGNLVTRPCDVKDE	299								
QY	301	TYDLLVQCDQAQPGASGYVYVWRKQKQKWKRIIGIFSGHQWDMNGSPDENVAVR	360								
DB	300	TYDLLVQCDQAQPGASGYVYVWRKQKQKWKRIIGIFSGHQWDMNGSPDENVAVR	359								
QY	361	ITPLKYAQICYWKGNVLDREG 383									
DB	360	ITPLKYAQICYWKGNVLDREG 382									
RESULT 4											
Q8BZS4	PRELIMINARY; PRT; 382 AA.										
ID	Q8BZS4										
AC	Q8BZS4										
DT	01-MAR-2003	(TEMBLrel. 23, Created)									
DT	01-MAR-2003	(TEMBLrel. 23, Last sequence update)									
DT	01-MAR-2004	(TEMBLrel. 26, Last annotation update)									
DE	Mus musculus adult male cecum cDNA, RIKEN full-length enriched										
DE	library, clone:9130215B18 product:SERINE PROTEASE (HYPOTHETICAL 43.0										
DE	kDa PROTEIN) (PROTEASE, SERINE, 23) homolog.										
OS	Mus musculus (Mouse).										
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;										
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.										
OX	NCBI_TaxId=10090;										
RN	[1]										
RP	SEQUENCE FROM N.A.										
RC	STRAIN=C57BL/6J; TISSUE=Cecum;										
RX	MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;										
RA	Carninci P., Hayashizaki Y.;										
RT	"High-efficiency full-length cDNA cloning.";										
RL	Meth. Enzymol. 303:19-44(1999).										
RN	[2]										
RP	SEQUENCE FROM N.A.										
RC	STRAIN=C57BL/6J; TISSUE=Cecum;										
RX	MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;										
RA	RIKEN FANTOM Consortium;										
RT	"Functional annotation of a full-length mouse cDNA collection.";										
RL	Nature 409:685-690(2001).										
RN	[3]										
RP	SEQUENCE FROM N.A.										
RC	STRAIN=C57BL/6J; TISSUE=Cecum;										
RA	The FANTOM Consortium;										
RT	"Analysis of the mouse transcriptome based on functional annotation of										
RT	60,770 full-length cDNAs.";										
RL	Nature 420:563-573(2002).										
SEQUENCE FROM N.A.											
STRAIN=C57BL/6J; TISSUE=Cecum; DOI=10.1101/gr.145100;											
MEDLINE=20499374; PubMed=11042159;											
Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,											
Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;											
"Normalization and subtraction of cap-trapper-selected cDNAs to											
prepare full-length cDNA libraries for rapid discovery of new genes.";											
Genome Res. 10:1617-1630(2000).											
[5]											
SEQUENCE FROM N.A.											
STRAIN=C57BL/6J; TISSUE=Cecum;											
MEDLINE=20330913; PubMed=11076861; DOI=10.1101/gr.152600;											
Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,											
Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M.,											
Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,											
Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,											
Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Watabiki M.,											
Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,											
Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;											
"RIKEN integrated sequence analysis (RISA) system-384-format											
sequencing pipeline with 384 multicapillary sequencer.";											
Genome Res. 10:1757-1771(2000).											
[6]											
SEQUENCE FROM N.A.											
STRAIN=C57BL/6J; TISSUE=Cecum;											
Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,											
Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,											
Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,											
Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,											
Kurihara C., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,											
Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,											
Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,											
Tagawa A., Takahashi F., Takaku-Akai H., Tanaka Y., Tanaka T.,											
Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;											
Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.											
-!- SIMILARITY: Belongs to peptidase family S1.											
DR	EMBL; AK033671; BAC28420.1; -.										
DR	GO; GO:0004263; F:chymotrypsin activity; IEA.										
DR	GO; GO:0008233; F:peptidase activity; IEA.										
DR	GO; GO:0004293; F:trypsin activity; IEA.										
DR	GO; GO:0006508; P:proteolysis and peptidolysis; IEA.										
DR	InterPro; IPR001254; Peptidase S1.										
DR	InterPro; IPR001314; Peptidase SLA.										
DR	InterPro; IPR009003; Pept Ser Cys.										
DR	PRINTS; PR00722; CHYMOTRYPSIN.										
DR	SMART; SM00020; Tryp_Spc; 1.										
DR	PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN 1.										
KW	Hydrolase; Hypothetical protein; Protease; Serine protease.										
SQ	SEQUENCE 382 AA; 43147 MW; 556789818E12A081 CRC64;										
Query Match 88.1%; Score 1860.5; DB 2; Length 382;											
Best Local Similarity 89.6%; Pred. No. 1.7e-156;											
Matches 343; Conservative 14; Mismatches 25; Indels 1; Gaps 1;											
QY	1	MAGIPGLLFLFLLCAVGQVSPYAPWKPPTWPAVRLPVVLPQSTLNLAQDFGAEAKLE	60								
DB	1	MAGIPG-LFILLVLLCVFMQVSPYTPWKPPTWPAVRLPVVLPQSTLNLAQDFDAKLE	59								
QY	61	VSSSCGPGCHKTPLPTTYKEAQYLSYETLYANGSRTXQVGIYILSSSGDGAXXRDSGS	120								
DB	60	VSSSCGPGCHKTPLPTTYEAAQYLSYETLYANGSRTXQVGIYILSSSGDGAXXRDSGA	119								
QY	121	SGKSRKRIQYGYDSRFSIFGKDFLLNYPFSTSVKLSCTGCTGLVAEXHVLTAACHIDG	180								
DB	120	TGSRKRIQYGYDSRFSIFGKDFLLNYPFSTSVKLSCTGCTGLVAEXHVLTAACHIDG	179								
QY	181	KTYVKGTQKLRLVGLFKPKFQKGGRGANDSTSAMPEQMKFQIRVKTHTVPGWIKGNAND	240								
DB	180	KTYVKGTQKLRLVGLFKPKYKDGAGDNSSSSAMPDKMKFQIRVKTHTVPGWIKGNAND	239								

[illegible]

Db 298 TIKOMPGBMTIHFSGDFNDRADQLVYRFCVSDESNLLLYQVCDAESGTSYGVLRLKDP 357
:::| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

Qy 328 QOQKWRIKIIFIGSHOWDMNGSPDNPVAVRITPLKYAQICWIKGNLYLDREG 383
:::| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

Db 358 DKONWKKTIAVYSGHQWDVGQKDYNVAVRITPLKYAQICLHIGNDANCAYG 413
:::| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

RESULT 6 .
QBNS320 PRELIMINARY; PRT; 413 AA.
AC QBNS320
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBurel. 22, Last sequence update)
DT 25-OCT-2004 (TrEMBurel. 28, Last annotation update)
DN Hypothetical protein PRSS35 [ENML522].
GE Name=PRSS35; ORFNames=UNQ522;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marzina K., Farmer A.A., Rubin G.M., Hong L.,
RA Scapellato M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Uesdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield V.S.,
RA Krzywinski M.I., Skalska U., Smalls D.E., Scherch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences."
RT Proc. Natl. Acad. Sci. U.S.A. 99:16999-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RA Strausberg R.;
RN Submitted (SEP-2002) to the EMBL/GenBank/DDBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=22887296; PubMed=12975309; DOI=10.1101/gr.1293003;
RA Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D., Brush J.,
RA Chen J., Chow B., Choi C., Crowley C., Currell B., Devel B., Dowd P.,
RA Eaton D., Foster J., Grimaldi C., Gu Q., Hass P.E., Heldens S.,
RA Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,
RA Lewis L., Liao D., Mark M., Robbie E., Sanchez C., Schoenfeld J.,
RA Sehgiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A.,
RA Vandlen R., Watanabe C., Wiand D., Woods K., Xie M.H., Yansura D.,
RA Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I.,
RA Godowski P.;
RT "The secreted protein discovery initiative (SPDI), a large-scale
effort to identify novel human secreted and transmembrane proteins: a
bioinformatics assessment.";
RT Genome Res. 13:2265-2270(2003).
CC -!- SIMILARITY: Belongs to peptidase family S1.
DR ENBL: BC037170; AAA37170.1;-
DR ENBL: AY358661; AAC89024.1;-
DR GO: GO:0004263; F:chymotrypsin activity; IEA.
DR GO: GO:0008233; F:peptidase activity; IEA.
DR GO: GO:0044295; F:tryptsin activity; IEA.
DR GO: GO:0006508; P:proteolysis and peptidolysis; IEA.


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RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
CC -I- SIMILARITY: Belongs to peptidase family S1.
DR EMBL; AK031411; BAC27392.1;
DR EMBL; BC075675; AAH75675.1;
DR MGD; MGI:2444800; P8835.
DR GO; GO:0005615; C:extracellular space; TAS.
DR InterPro; IPR001254; Peptidase_S1.
DR InterPro; IPR001314; Peptidase_S1A.
DR InterPro; IPR009003; Pept_Ser_Cys.
DR Pfam; PF00089; Trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR SMART; SM00020; Tryp_SPC; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.
DR HydroLase; Protease; Serine protease.
KW SEQUENCE 409 AA; 45787 MW; 5E22D4A908E7EPE5 CRC64;

Query Match 47.5%; Score 1003.5; DB 2; Length 409;
Best Local Similarity 48.8%; Pred. No. 2.1e-80;
Matches 191; Conservative 68; Mismatches 85; Indels 47; Gaps 5;

QY 31 TWPAYRLPVLPVLPSTLNLAKEPFGAEAKLEVSSCGPQCHGCTPLPTYPEAKQYLSYETL 90
DB 28 TWHLRSRIPQVVSNTIHLASPTFQADAGVVKATVCGIECOEELPAPSLQLESLSYETI 87

QY 91 YANGSRTEKXQGVYIL-----SSSGDGAAXRDSGSGKRRKQIYGYDSRFSIFGKDF 144
DB 88 FENGTRILTRVQGLVLETRNSVKG-----HPRRRQVGTDSRFSILDKRF 138

QY 145 LLNYPFSTSVKLTGCTGTLVAEXHVLTAACHDGVYKGTQKLVGFLKPKFDG-- 202
DB 139 ATNFPNTAVKLTGCGTGLVSPNHVLTAAHCHVDGKDYVKGSKLVRVGLKVRNKGGR 198

QY 203 -GGA-----NDSTSAMPEQM-----KFWIRVGRTHVPKG 232
DB 199 KRGSKRSRREAESAGSQAHLESTTQRPCKSRGRPRVTQGRPSQWTRVKSHTPKG 258

QY 233 WIKGNANDIGMDYDVALLELKKPKFKMIGVSPPAKQLPGRIHFGSYDNDRPGNLVY 292
DB 259 WVGENGGLALDYDVALLELKRHKQHMELGVSPITKLPGRRIHFGFDNDRDQLVY 318

QY 293 RFDVDRDEYDLYQQCDAGQASGAGSYGVYVMWKQKQKWERKIIGFSGHGWDMNGSP 352
DB 319 RFCSVSEESNDLYQYCDABAGSTGSGIYLRLEKPEQKWKRIYAVYSGHQVDVHGQV 378

QY 353 QDPNVAVRITPLKYAQICVYKIGNYLDREG 383
DB 379 KDYNVAVRITPLKYAQICLWIHGNAANCAYG 409

RESULT 8
Q8COL5 PRELIMINARY; PRT; 409 AA.
AC Q8COL5;
DT 01-MAR-2003 (T-EMBLrel. 23, Created)
DT 01-MAR-2003 (T-EMBLrel. 23, Last sequence update)
DT 01-MAR-2004 (T-EMBLrel. 26, Last annotation update)
DE Mus musculus 6 days neonate head cDNA, RIKEN full-length enriched
DE library, clone:5430417J04 product:similar to DJ223E3.1 (PUTATIVE
DE SECRETED PROTEIN ZS1G13), full insert sequence.
GN Names=Prs35;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Head;
RX MEDLINE=99279233; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA Carninci P., Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning.";
RL Meth. Enzymol. 303:19-44(1999).
RN [2]
RP SEQUENCE FROM N.A.

STRAIN=C57BL/6J; TISSUE=Head;
MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RIKEN PANTOM Consortium;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Head;
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Head;
RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA Konno H., Okazaki Y., Muratsu M., Hayashizaki Y.;
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
RT prepare full-length cDNA libraries for rapid discovery of new genes.";
RL Genome Res. 10:1617-1630(2000).
RN [5]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Head;
RX MEDLINE=1076861; DOI=10.1101/gr.152600;
RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA Konno H., Akiyama Y., Nishi K., Kitsunai T., Tashiro H., Itoh M.,
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA Fujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
RA Okazaki Y., Muratsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system-384-Format
RT sequencing pipeline with 384 multicapillary sequencer.";
RL Genome Res. 10:1757-1771(2000).
RN [6]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Head;
RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
RA Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
RA Hori F., Inotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
RA Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,
RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
RA Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
RA Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
RA Tomaru A., Toya T., Yasunishi A., Muratsu M., Hayashizaki Y.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
CC -I- SIMILARITY: Belongs to peptidase family S1.
DR EMBL; AK030671; BAC27073.1;
DR MGD; MGI:2444800; P8835.
DR GO; GO:0005615; C:extracellular space; TAS.
DR InterPro; IPR001254; Peptidase_S1.
DR InterPro; IPR001314; Peptidase_S1A.
DR InterPro; IPR009003; Pept_Ser_Cys.
DR Pfam; PF00089; Trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR SMART; SM00020; Tryp_SPC; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.
KW HydroLase; Protease; Serine protease.
KW SEQUENCE 409 AA; 45847 MW; ASAC1C582BFD352E CRC64;

Query Match 47.3%; Score 998.5; DB 2; Length 409;
Best Local Similarity 48.6%; Pred. No. 5.8e-80;
Matches 190; Conservative 68; Mismatches 86; Indels 47; Gaps 5;

QY 31 TWPAYRLPVLPVLPSTLNLAKEPFGAEAKLEVSSCGPQCHGCTPLPTYPEAKQYLSYETL 90
DB 28 TWHLRSRIPQVVSNTIHLASPTFQADAGVVKATVCGIECOEELPAPSLQLESLSYETI 87

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QY 91 YANGSRTEXOVGIYIL-----SSSGDGAAXXRDSSGSKRRKQIYGYDVSRSIFGKDF 144
Db FENGTRTLLKQVQLLEPTNRSSVKG-----HPRRRQYVGTDSRESILDKRF 138
QY 145 LLNVPSTSVKLSGCTGLVAEXHVLTAACHIDGKTVYKGTOKLVRGPKLKFYKDG-- 202
Db 139 ATNFPFNIAVLSTGCGSTGLVSNHVLTAACHVDGKDYVYKSGKLRVGLKRNKGGRR 198
QY 203 -GRGA-----NDSTSAMPEQM-----KQWIRVVRKTHVPKG 232
Db 199 KRGSKESREAESAGOSQAHLESITQRPCKSRGPRVTVQGRPSFQWTRVKSITHPKG 258
QY 233 WIKGNANDIGMDYDYLLELKKPKHFKMIGVSPPAKQLPGRIHFSQYDNDRPNLVY 292
Db 259 WVRGSGSLDLYDYLLELKRHAKHQHMLGVSPTITKLPGRIHFSQYDNDRDLQVY 318
QY 293 RFDVNDKTDLYLQCDQAOPGASGVYVYRWKROQKWKRIIGFSQHWVDMNGSP 352
Db 319 RFGVSSESNLLYQYCDAGSTGSGIYLRKPEQGNKWKRIYAVISGHQWVDVHGQ 378
QY 353 QDNVAVRITPLKYAQICWYKIGNYLDCREG 383
Db 379 KDYNVAVRITPLKYAQICLWIHGNAACVAG 409
RESULT 9
Q6GML6 PRELIMINARY; PRT; 418 AA.
AC Q6GML6
DT 05-JUL-2004 (TREMBLrel. 27, Created)
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
DE zgc:91804.
GN ORFNames=zgc:91804;
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=whole;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Scapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Uadin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Heiton E., Ketterman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalka U., Smallos D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=whole;
RX Strausberg R.;
DR ENBL; BC074028.1;
DR ZFIN; ZDB-GENE-040704-55; zgc:91804.
DR GO; GO:0008233; F:peptidase activity; IEA.
DR GO; GO:0004295; F:trypsin activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.

DR InterPro; IPR001254; Peptidase_S1.
DR InterPro; IPR009003; Pept_Ser_Cys.
DR Pfam; PF00089; Trypsin; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.
KW Hydrolase; protease; Serine protease
SQ SEQUENCE 418 AA; 47270 MW; AF33345CEB94F720 CRC64;
Query Match 47.1%; Score 994.5; DB 2; Length 418;
Best Local Similarity 45.8%; Pred. No. 1.3e-79;
Matches 193; Conservative 63; Mismatches 122; Indels 43; Gaps 2;
QY 1 MAGIFGLLPLFLCAVQVSPYAPWKPWPAVRLPVVLQSTLNLAQPFQGAQKLE 60
Db 1 MGPEVLTLLLSALAVLGSTTVDDPTGDTWTPQRIPLVQEKQTVHLESSEFLAKPOND 60
QY 61 VSSSGCPQCHKGTPLPTYPEAKQYLSYETLYANGSRTEXQVGIYILSSSGDGAAXXRDSSG 120
Db 61 LHGIGIECOQLRPLPSLDLLEQLLSYETWYDNGTRTLTTVTVDLNVNDWT-----GAS 116
QY 121 SGKSRKRQIYGYDSRFSIFGKDFLLNYPFSTSVKLSGCTGLVAEXHVLTAACHIDG 180
Db 117 QLHTRHREVYGTDRFTITDKQYSKYPFSTSVKISTGSGVLVSPKHVLTAAHCHHG 176
QY 181 KTYVGTOKLVRGFLKP-----KFKD 201
Db 177 TDYLDGVQKLSVGLKERSRRKNGRKGKRGKQKHHEEEVDENGEIVEQQRKSKG 236
QY 202 GGRGANDSTSAMPEOMKQWIRVVRKTHVPKWIKGNANDIGMDYDYLLELKKPKHKKFM 261
Db 237 KGRNRSRSTDSQSPFRWTRVQKQVFKGFKGISENLADYAVLELRAQTKFM 296
QY 262 KIGVSPPAKQLPGRHFSQYDNDRPNLVRFCVDFKDTYDLYLQCDQAOPGASGVY 321
Db 297 DLGVIPSVKCLPAGRIHFSQYDNDRPNLVRFCVDFKDTYDLYLQCDQAOPGASGVY 356
QY 322 VRMVTRQOKWKRIIGFSQHWVDMNGSPDFVAVRITPLKYAQICWYKIGNYLDRCR 381
Db 357 IRLKEPFGKKKWKRIIGVFSQHWVDMNGSPDFVAVRITPLKYAQICWYKIGNYLDRCR 416
QY 382 E 382
Db 417 D 417
RESULT 10
Q8COD6 PRELIMINARY; PRT; 409 AA.
ID Q8COD6
AC Q8COD6; (TREMBLrel. 23, Created)
DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE Mus musculus 13 days embryo male testis cDNA, RIKEN full-length
DE enriched library clone:603046M24 product:similar to DJ223E3.1
DE (PUTATIVE SECRETED PROTEIN ZS1G13), full insert sequence.
GN Name=Pras35;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Testis;
RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA Carninci P., Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning."
RL Meth. Enzymol. 303:19-44(1999).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Testis;
RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA RIKEN FANTOM Consortium;
RT "Functional annotation of a full-length mouse cDNA collection."
RL Nature 409:685-690(2001).

RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Testis;
 RA The FANTOM Consortium,
 RA the RIKEN Genome Exploration Research Group Phase I & II Team;
 RT "Analysis of the mouse transcriptome based on functional annotation of
 RT 60,770 full-length cDNAs";
 RL Nature 420:563-573(2002).
 RN [4]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Testis;
 RX MEDLINE=20493374; PubMed=11042159; DOI=10.1101/gr.145100;
 RA Carninci P., Shibata Y., Hayatsu M., Sugahara Y., Shibata K., Itoh M.,
 RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.,
 RT "Normalization and subtraction of cap-trapper-selected cDNAs to
 RT prepare full-length cDNA libraries for rapid discovery of new genes";
 RL Genome Res. 10:1617-1630(2000).
 RN [5]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Testis;
 RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
 RA Shibata K., Itoh M., Aizawa K., Nagao S., Sasaki N., Carninci P.,
 RA Konno H., Akiyama J., Nishi K., Kiteunai T., Tashiro H., Itoh M.,
 RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
 RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
 RA Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Watabiki M.,
 RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
 RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
 RT "RIKEN integrated sequence analysis (RISA) system-384-format
 RT sequencing pipeline with 384 multicapillary sequencer";
 RL Genome Res. 10:1757-1771(2000).
 RN [6]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Testis;
 RA Adachi J., Aizawa K., Akamura T., Arakawa T., Bono H., Carninci P.,
 RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
 RA Hayashida K., Hayatsu N., Hiramoto K., Hizaoka T., Hirozane T.,
 RA Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
 RA Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,
 RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
 RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
 RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
 RA Sasaki D., Shibata K., Shingawa A., Shiraki T., Sogabe Y., Tagami M.,
 RA Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
 RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AK031644; BAC27491.1; -;
 DR MGD; MGI:2444800; Prs635.
 DR GO; GO:0005615; C:extracellular space; TAS.
 DR InterPro; IPR001254; Peptidase_S1.
 DR InterPro; IPR009003; Pept_Ser_Cys.
 DR Pfam; PF00089; Trypsin; 1.
 DR SMART; SM00020; Tryp_SPC; 1.
 KW Hydrolase; Protease; Serine protease.
 SQ SEQUENCE 409 AA; 45736 MW; B9C9B9B1E6800719C CRC64;
 Query Match 47.0%; Score 992.5; DB 2; Length 409;
 Best Local Similarity 48.3%; Pred. No. 2e-79;
 Matches 189; Conservative 70; Mismatches 85; Indels 47; Gaps 5;
 QY 31 TWPAYLPVVLPOSTLNLAKPDFGAELKLEVVSSCGPQCHGTPLPTYPEAKQYLSYETL 90
 DB 28 TWHLRIQVSVSTLHSLASPTQADGVVYKATVCIGEQEELPAPSLSQLESLEYETI 87
 QY 91 YANGSRTEQVGYIL-----SSSDGAXKRDSSGSGKRRKQIYGVDSRFSIFGKDF 144
 DB 88 FENGTRTLRVKQGLVLETRNSVKG-----HPRRRQVYGTDSRFSILDKPF 138
 QY 145 LNNYPTSTSVKLTGCTGTVAEXHVLTAACHDGTYYVKGQKLRVGLPKFPGD-- 202
 DB 139 ATNFPNTAVKLTGCGSLTSPNHLTAANCVDHGDYVKGSKLRLVGLKRNKGRK 198
 QY 203 -GRGA-----NDSTSAMPEQM-----KFWIRVKTHTVPKG 232

DB 199 KRGSKRSRREAESAGSOAHLRESITTPQPKSRREGPRVTQGRPSFQWTRVKSHTPKG 258
 QY 233 WIKGNANDIGMDYVYALLELKPKHKKFKMIGVSPPAKQLPGRIHPSGVDNDRPGLVY 292
 DB 259 WRGEGGLDLYDYALLELKRAHKQHMELGVSPTITKLPQGGIHFSGFDNRDEQLVY 318
 QY 293 RFGCDVKDLYDLYLQCDAPGASGVVYVVMKROQKWKRIIGIFSGHGVNDKNSP 352
 DB 319 RFGVSEESNDLYQYCDABAGSTGSGIYRLKPEQCKWKRKIYAVYSGHQWVDVHGQV 378
 QY 353 QDFNVAVRITPLKYAQICWIKGNYLDCREG 383
 DB 379 KDYNVAVRITPLKYAQICLWIHGNAANCAVG 409
 RESULT 11
 GSEP_BACLI
 ID GSEP_BACLI STANDARD; PRT; 316 AA.
 AC P80057;
 DT 01-MAY-1992 (Rel. 22, Created)
 DT 01-OCT-1993 (Rel. 27, Last sequence update)
 DT 25-OCT-2004 (Rel. 45, Last annotation update)
 DE Glutamyl endopeptidase precursor (EC 3.4.21.19) (Glutamate specific
 endopeptidase) (GSE).
 GN Name:blase;
 OS Bacillus licheniformis.
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
 OX NCBI_TaxID=1402;
 [1] SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
 RP STRAIN=ATCC 14580;
 RC MEDLINE=93054737; PubMed=1429718;
 RA Kakudo S., Kikuchi N., Kitadokoro K., Fujiwara T., Nakamura E.,
 RA Okamoto H., Shin M., Tanaki M., Teraoka H., Tsuzuki H., Yoshida N.;
 RT "Purification, characterization, cloning, and expression of a glutamic
 RT acid-specific protease from Bacillus licheniformis ATCC 14580";
 RL J. Biol. Chem. 267:23782-23788(1992).
 RN [2]
 RP SEQUENCE OF 95-316.
 RX MEDLINE=92155199; PubMed=1346764;
 RA Svendsen I., Breddam K.;
 RT "Isolation and amino acid sequence of a glutamic acid specific
 RT endopeptidase from Bacillus licheniformis";
 RL Eur. J. Biochem. 204:165-171(1992).
 CC -!- FUNCTION: Specific for hydrolysis of peptide bonds on the carboxyl
 CC side of acidic amino acid residues, with a strong preference for
 CC Glu.
 CC -!- CATALYTIC ACTIVITY: Preferential cleavage: Asp|-Xaa, Glu|-Xaa.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- SIMILARITY: Belongs to the peptidase S1B family.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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 CC or send an email to license@sib-sib.ch).
 CC -----
 CC EMBL; D10060; BAA00949.1; -;
 DR FIR; A45134; A45134.
 DR MEROPS; S01.271; -;
 DR InterPro; IPR00126; Pept_S1B_AS.
 DR InterPro; IPR009003; Pept_Ser_Cys.
 DR InterPro; IPR001254; Peptidase_S1.
 DR InterPro; IPR008256; Peptidase_S1B.
 DR Pfam; PF00089; Trypsin; 1.
 DR PRINTS; PR00839; V8PROTEASE.
 DR SMART; SM00020; Tryp_SPC; 1.
 DR PROSITE; PS00672; V8_HIS; 1.
 DR PROSITE; PS00673; V8_SER; 1.
 KW Direct protein sequencing; Hydrolase; Serine protease; Signal.

[illegible]

03-JUL-2004 (TREMblrel. 27, Last sequence update)
 DT DE Serine protease, putative.
 DN OrderedLocusNames=LMOF2365_1900;
 GN Listeria monocytogenes (serotype 4b / strain F2365).
 OS Bacteria; Firmicutes; Bacillales; Listeriaceae; Listeria.
 NCBI_TaxID=565669;
 RX [1]
 RN
 RP SEQUENCE FROM N.A.
 RX PubMed=15115801; DOI=10.1093/nar/gkh562;
 RA Nelson K.E., Fouts D.E., Mongodin E.F., Ravel J., DeBoy R.T.,
 RA Kelanay J.F., Rasko D.A., Angiuoli S.V., Gill S.R., Paulsen I.T.,
 RA Peterson J.D., White O., Nelson W.C., Nierman W.C., Beanan M.J.,
 RA Brinkac L.M., Daugherty S.C., Dodson R.J., Durkin A.S., Madupu R.,
 RA Haft D.H., Selengut J., Van Aken S.E., Khouri H.M., Fedorova N.,
 RA Forbarger H.A., Tran B., Kathariou S., Wonderling L.D., Uhlrich G.A.,
 RA Bayles D.O., Luchanov J.B., Fraser C.M.;
 RT "Whole genome comparisons of serotype 4b and 1/2a strains of the food-
 RT borne pathogen *Listeria monocytogenes* reveal new insights into the
 RT core genome components of this species.";
 RL Nucleic Acids Res. 32:23386-23395(2004).
 DR EMBL: AS017328; AAT04669.1; -
 DR GO: GO:0004295; F-trypsin activity; IEA.
 DR GO: GO:0006508; P:proteolysis and peptidolysis; IEA.
 DR InterPro: IPR006637; Chw.
 DR InterPro: IPR001254; Peptidase_S1.
 DR InterPro: IPR008256; Peptidase_S1B.
 DR InterPro: IPR009003; Pept_Ser_Cys.
 DR Pfam: PF07538; Chw; 3.
 DR PRINTS: PR00839; VAPROTEASE.
 DR SMART: SM00728; Chw; 3.
 DR PROSITE: PS02440; TRYPSIN_DOM; 1.
 DR PROSITE: PS00134; TRYPSIN_HIS; UNKNOWN_1.
 KW Complete proteome; Hydrolase; Protease; Serine protease.
 SQ SEQUENCE 450 AA; 48793 MW; 54C79A67510FAD4A CRC64;

Query Match		8.6%;	Score 182;	DB 2;	Length 450;
Best Local Similarity		25.6%;	Pred. No. 1.8e-07;		
Matches		69;	Conservative	43;	Mismatches 86; Indels 72; Gaps 13;
Qy	128	ROIYGYDSRFSIFGKDFLLN---	YPFSTS	-----VKLS	GTGCT-----GTLVAEXHVLTAHC 176
Db	93	KTIFFGGD	-----GRKLVTNTQTPYSTSA	YLVMEFPNGKTYIGSGQLIGSDSVLTAHC 146	
Qy	177	IHDGKTYVKGTKLRVGLPKPKFDGG	-----RGANDSTS	SAMPEQMKFQWIRVKRTH 228	
Db	147	LY-GK	-----KDGWAKKVTVYPGNGT	-----KAPGTAKAKGWY 181	
Qy	229	VPKGIWIKGNANDIGMDYDYLLEKLPKHKFKMIGVSPPAKQLPGRHIFSGYDNRPG	288		
Db	182	VPKEWTKKEPS	-----TEDYGVIKLDKNIKTGTGTWGLTNT	-----SGAITTISYGHGDKKG 233	
Qy	289	NLVYRFDCKVDKDETYDLYQOCDAQPGASGYGVYVWMKROOKWERKLIIGTIFSGHQWDM	348		
Db	234	KLYTQTGNISQVANNFYRLDTTGGSSGSGVY	-----NSKQILAV-NAYEYLNG 289		
Qy	349	NGSPQDFNVAVRITPLKYAICYWIKGNYL	378		
Db	284	TGD	-----NFGTRITKEXLNNIYTWAFDNNL 309		
RESULT 14					
Q98GI7	PRELIMINARY; PRT; 364 AA.				
ID	Q98GI7				
AC	Q98GI7				
DT	01-OCT-2001 (TrEMBLrel. 18, Created)				
DT	01-OCT-2001 (TrEMBLrel. 18, Last sequence update)				
DT	01-MAR-2004 (TrEMBLrel. 26, Last annotation update)				
DE	Glutamyl endopeptidase (EC 3.4.21.19).				
GN	OrderedLocusNames=ml13306;				
OS	Rhizobium loti (Mesorhizobium loti).				
OC	Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;				
OC	Phyllobacteriaceae; Mesorhizobium.				
ON	NCBI_TaxID=381;				
OX	[1]				
RP	SEQUENCE FROM N.A.				
RC	STRAIN=MAFF303039;				
RX	MEDLINE=21082930; PubMed=11214968;				
RA	Kaneko T., Nakamura Y., Sato S., Asamizu E., Kato T., Sasamoto S.,				
RA	Watanabe A., Idegawa K., Ishikawa A., Kawashima K., Kimura T.,				
RA	Kishida Y., Kiyokawa C., Kohara M., Matsuoto M., Matsuoto A.,				
RA	Mochizuki Y., Nakayama S., Nakazaki N., Shimpo S., Sugimoto M.,				
RA	Takeuchi C., Yamada M., Tabata S.;				
RT	"Complete genome structure of the nitrogen-fixing symbiotic bacterium				
RT	Mesorhizobium loti."				
RL	DNA Res. 7:331-338(2000).				
RL	EMBL; AP003001; BAB50229.1; -				
DR	GO; GO:0004295; F:tryptase activity; IEA.				
DR	GO; GO:0006508; P:proteolysis and peptidolysis; IEA.				
DR	InterPro; IPR001254; Peptidase_S1.				
DR	InterPro; IPR008256; Peptidase_S1B.				
DR	InterPro; IPR009003; Pept_Ser_Cys.				
DR	Pfam; PF00089; Trypsin; 1.				
DR	PRINTS; PR00839; V8PROTEASE.				
DR	SMART; SM00020; Tryp_SPC; 1.				
DR	PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.				
KW	Complete proteome; Hydrolase; Protease; Serine protease.				
SQ	SEQUENCE 364 AA; 39034 MW; 13BE653270E7CDD3 CRC64;				
Query Match					
Best Local Similarity 7.8%; Score 165.5; DB 2; Length 364;					
Matches 77; Conservative 41; Mismatches 117; Indels 53; Gaps 16;					
Qy	107	SSSGDGAXXR-DGSSGSKRRKRIQYGYDSRFSIFGKDFLLNYPFST	-----SVKLST 158		
Db	112	ANGADGAERTDEPGLGEAGEAGRVFPDDRQVRNTK	---TVPFSAIGYLEAKS	AKTGS 168	
Qy	159	--GCTGTLVAEXHVLTAHC	CI--HDGKTYVKGTKLRVGLPKPKFDGGRGANDSTS	SAMP 214	

Oy 324 MWKRQQQKWKIIGI-----FSGHQWVDMNGSPQD-----PNVAVRITP 363
Db 210 -WIHRQQAGPPVIVAVHTAGPRPHSGGAWGCRPGVPLAPAGLFNRCVRLTP 259

Search completed: July 1, 2005, 21:08:10
Job time : 96.7095 secs

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OM protein - protein search, using sw model

Run on: July 1, 2005, 20:52:53 ; Search time 100.435 Seconds
(without alignments)
1509.530 Million cell updates/sec

Title: US-09-658-677-15
Perfect score: 2131
Sequence: 1 MAGIPGLFLFLFLCAVQ.....IKGNVLDRCGDTVPFPGSN 392

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_16Dec04:*
1: Geneseq1980s:*
2: Geneseq1990s:*
3: Geneseq2000s:*
4: Geneseq2001s:*
5: Geneseq2002s:*
6: Geneseq2003as:*
7: Geneseq2003bs:*
8: Geneseq2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Query Length	ID	Description
1	2131	100.0	392	4	AAB48973 Human Zsi
2	2085	97.8	392	4	AAB48972 Human Zsi
3	2080	97.6	383	2	AAY08660 WO9927094
4	2080	97.6	383	2	AAY08657 Human tra
5	2080	97.6	383	2	AAY13390 Amino aci
6	2080	97.6	383	3	AAY88277 Human TAN
7	2080	97.6	383	3	AAY87270 Human sig
8	2080	97.6	383	3	AAY53627 A bone ma
9	2080	97.6	383	3	AAB25618 Protein e
10	2080	97.6	383	3	AAB25592 Protein e
11	2080	97.6	383	3	ADC78573 Human PRO
12	2080	97.6	383	4	AAB80258 Human PRO
13	2080	97.6	383	4	AAB48974 Human Zsi
14	2080	97.6	383	4	AAB29048 Human PRO
15	2080	97.6	383	6	ABU58424 Human PRO
16	2080	97.6	383	6	ABU71636 Human PRO
17	2080	97.6	383	6	ABU87972 Novel hum
18	2080	97.6	383	6	ABU84287 Human sec
19	2080	97.6	383	6	ABR56161 Human sec
20	2080	97.6	383	6	ABR65551 Human sec
21	2080	97.6	383	6	ABU99491 Human sec
22	2080	97.6	383	6	ABU82730 Human PRO
23	2080	97.6	383	6	ABU89851 Novel hum
24	2080	97.6	383	6	ABU71491 Human PRO
25	2080	97.6	383	6	ABR68100 Human sec

26	2080	97.6	383	6	ABU96153	Novel hum
27	2080	97.6	383	6	ABU92584	Human sec
28	2080	97.6	383	6	ABO08661	Human sec
29	2080	97.6	383	6	ABO02713	Human sec
30	2080	97.6	383	6	ABR74867	Human sec
31	2080	97.6	383	6	ABR94629	Human sec
32	2080	97.6	383	6	ABU85602	Human PRO
33	2080	97.6	383	6	ABU98762	Novel hum
34	2080	97.6	383	6	ABU97977	Novel hum
35	2080	97.6	383	6	ABU91683	Novel hum
36	2080	97.6	383	6	ABU71937	Human sec
37	2080	97.6	383	6	ABU89376	Human PRO
38	2080	97.6	383	6	ABU86217	Human sec
39	2080	97.6	383	6	ABU67430	Human sec
40	2080	97.6	383	6	ABU80458	Human PRO
41	2080	97.6	383	6	ABO01820	Novel hum
42	2080	97.6	383	6	ABR99376	Human sec
43	2080	97.6	383	6	ABR98766	Human sec
44	2080	97.6	383	6	ABO16289	Human sec
45	2080	97.6	383	6	ABR92189	Human sec

ALIGNMENTS

RESULT 1
AAB48973
ID AAB48973 standard; protein; 392 AA.
XX AAB48973;
AC
XX 27-MAR-2001 (first entry)
DT
XX
DE Human Zsig13 variant #2, SEQ ID NO:15.
XX
KW Human Zsig13; serine protease; chromosome 11q22.1; elastase homologue;
KW glucamyl endopeptidase homologue; factor X homologue; trypsin homologue;
KW trypsinogen homologue; mast cell protease homologue;
KW collagenase homologue; protein degradation; food processing; brewing;
KW alcohol production; laundry detergent component.
XX
OS Homo sapiens.
XX
XX US6153420-A.
XX
XX 28-NOV-2000.
XX
XX 04-MAY-1998; 98US-00072384.
XX
XX 24-APR-1997; 97US-0044185P.
XX 17-APR-1998; 98US-00062142.
XX (ZYMO) ZYMOGENETICS INC.
XX Sheppard PO;
XX
XX WPI; 2001-060090/07.
XX N-PSDB; AAC91783.
XX
XX New isolated serine protease (designated Zsig13), useful in industrial processes to degrade unwanted proteins or alter the characteristics of protein-containing composition, as well as in industrial applications (e.g. brewing).
XX
XX Claim 1; Col 35-38; 26pp; English.
XX
XX The invention relates to human Zsig13 proteins (AAB48972-B48974), and to DNA encoding them (AAC91782-C91784). The invention also relates to expression vectors and host cells comprising a human Zsig13 DNA, and the recombinant production of a human Zsig13 protein or its precursor. Zsig13 is a serine protease, and has significant homology to Bacillus licheniformis glutamyl endopeptidase, human clotting factor X, human elastase, rat mast cell protease, Streptomyces griseus trypsin, bovine

CC trypsinogen, and Hypoderma lineatum collagenase. The gene encoding human
CC Zsig13 is located on chromosome 11q22.1. Zsig13 is useful in industrial
CC processes to degrade unwanted proteins or alter the characteristics of
CC protein-containing compositions. It may also be used in industrial
CC applications in which proteases are utilised, including food processing,
CC brewing and alcohol production, and as a component of a laundry
CC detergent. The present sequence represents a human Zsig13 variant
XX
SQ Sequence 392 AA;

Query Match 100.0%; Score 2131; DB 4; Length 392;
Best Local Similarity 100.0%; Pred. No. 4.4e-151;
Matches 392; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAGIPGLLFLFLCAVGVSPYSAPWKPPTWPAAYRLPVVLPQSTLNLAKEPFGAEAKLE 60
Db 1 MAGIPGLLFLFLCAVGVSPYSAPWKPPTWPAAYRLPVVLPQSTLNLAKEPFGAEAKLE 60

QY 61 VSSSCGPQCHKGTPPTYEAKQYLSYETLYANGSRTEQVGIYILSSSGDGAQHRS DGS 120
Db 61 VSSSCGPQCHKGTPPTYEAKQYLSYETLYANGSRTEQVGIYILSSSGDGAQHRS DGS 120

QY 121 SGKSRKROIYGYDSRFSIFGKDFLLNYPFSTSVKLSGTCTGLVAEKHVLTAACHIDG 180
Db 121 SGKSRKROIYGYDSRFSIFGKDFLLNYPFSTSVKLSGTCTGLVAEKHVLTAACHIDG 180

QY 181 KTYVKGTKLRVGLFKPKFDGGRGANDSTSAPMEQKQWIRVKTTHVPKGIKNAND 240
Db 181 KTYVKGTKLRVGLFKPKFDGGRGANDSTSAPMEQKQWIRVKTTHVPKGIKNAND 240

QY 241 IGMVDYALLELKKPHKRFKMGIVSPPAKQLPGGRIHPSGYDNDPGLNLYRFCVDKDE 300
Db 241 IGMVDYALLELKKPHKRFKMGIVSPPAKQLPGGRIHPSGYDNDPGLNLYRFCVDKDE 300

QY 301 TYDLLYQCCDAQPGASGSGVYVVMKROQKWERKIIGIFSGHQMVDNMGSPDFNVAVR 360
Db 301 TYDLLYQCCDAQPGASGSGVYVVMKROQKWERKIIGIFSGHQMVDNMGSPDFNVAVR 360

QY 361 ITPLKYAQICYWIKGNLYDCREGDTVFPPGNS 392
Db 361 ITPLKYAQICYWIKGNLYDCREGDTVFPPGNS 392

RESULT 2
AAB48972
ID AAB48972 standard; protein; 392 AA.
AC AAB48972;
XX
XX
DT 27-MAR-2001 (first entry)
XX
XX Human Zsig13 variant #1, SEQ ID NO:2.
DE
DE Human Zsig13; serine protease; chromosome 11q22.1; elastase homologue;
KW glutamyl endopeptidase homologue; factor x homologue; trypsin homologue;
KW trypsinogen homologue; mast cell protease homologue;
KW collagenase homologue; protein degradation; food processing; brewing;
KW alcohol production; laundry detergent component.
XX
XX Homo sapiens.
OS
XX
XX US6153420-A.
XX
XX 28-NOV-2000.
XX
XX 04-MAY-1998; 98US-00072384.
XX
XX 24-APR-1997; 97US-0044185P.
PR 17-APR-1998; 98US-00062142.
XX
XX (ZYMO) ZYMOGENETICS INC.
PA
XX
XX Sheppard PO;
PI

XX
DR WPI; 2001-060090/07.
DR N-PSDB; AAC91782.
XX
XX New isolated serine protease (designated Zsig13), useful in industrial
PT processes to degrade unwanted proteins or alter the characteristics of
PT protein-containing composition, as well as in industrial applications
PT (e.g. brewing).
XX
XX Claim 1; Col 25-28; 26pp; English.
XX
XX The invention relates to human Zsig13 proteins (AAB48972-B48974), and to
CC DNA encoding them (AAC91782-C91784). The invention also relates to
CC expression vectors and host cells comprising a human Zsig13 DNA, and the
CC recombinant production of a human Zsig13 protein or its precursor. Zsig13
CC is a serine protease, and has significant homology to Bacillus
CC licheniformis glutamyl endopeptidase, human clotting factor X, human
CC elastase, rat mast cell protease, Streptomyces griseus trypsin, bovine
CC trypsinogen, and Hypoderma lineatum collagenase. The gene encoding human
CC Zsig13 is located on chromosome 11q22.1. Zsig13 is useful in industrial
CC processes to degrade unwanted proteins or alter the characteristics of
CC protein-containing compositions. It may also be used in industrial
CC applications in which proteases are utilised, including food processing,
CC brewing and alcohol production, and as a component of a laundry
CC detergent. The present sequence represents a human Zsig13 variant
XX
SQ Sequence 392 AA;

Query Match 97.8%; Score 2085; DB 4; Length 392;
Best Local Similarity 98.2%; Pred. No. 1.2e-147;
Matches 385; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 1 MAGIPGLLFLFLCAVGVSPYSAPWKPPTWPAAYRLPVVLPQSTLNLAKEPFGAEAKLE 60
Db 1 MAGIPGLLFLFLCAVGVSPYSAPWKPPTWPAAYRLPVVLPQSTLNLAKEPFGAEAKLE 60

QY 61 VSSSCGPQCHKGTPPTYEAKQYLSYETLYANGSRTEQVGIYILSSSGDGAQHRS DGS 120
Db 61 VSSSCGPQCHKGTPPTYEAKQYLSYETLYANGSRTEQVGIYILSSSGDGAQHRS DGS 120

QY 121 SGKSRKROIYGYDSRFSIFGKDFLLNYPFSTSVKLSGTCTGLVAEKHVLTAACHIDG 180
Db 121 SGKSRKROIYGYDSRFSIFGKDFLLNYPFSTSVKLSGTCTGLVAEKHVLTAACHIDG 180

QY 181 KTYVKGTKLRVGLFKPKFDGGRGANDSTSAPMEQKQWIRVKTTHVPKGIKNAND 240
Db 181 KTYVKGTKLRVGLFKPKFDGGRGANDSTSAPMEQKQWIRVKTTHVPKGIKNAND 240

QY 241 IGMVDYALLELKKPHKRFKMGIVSPPAKQLPGGRIHPSGYDNDPGLNLYRFCVDKDE 300
Db 241 IGMVDYALLELKKPHKRFKMGIVSPPAKQLPGGRIHPSGYDNDPGLNLYRFCVDKDE 300

QY 301 TYDLLYQCCDAQPGASGSGVYVVMKROQKWERKIIGIFSGHQMVDNMGSPDFNVAVR 360
Db 301 TYDLLYQCCDAQPGASGSGVYVVMKROQKWERKIIGIFSGHQMVDNMGSPDFNVAVR 360

QY 361 ITPLKYAQICYWIKGNLYDCREGDTVFPPGNS 392
Db 361 ITPLKYAQICYWIKGNLYDCREGDTVFPPGNS 392

RESULT 3
AAY08660
ID AAY08660 standard; protein; 383 AA.
XX
XX AAY08660;
XX
XX 09-AUG-1999 (first entry)
DT
XX
XX WO9927094 Seq ID 12.
DE
XX
XX Transmembrane domain; human; nutrition; cytokine; cell differentiation;
KW immune stimulation; immune suppression; haematopoiesis; activin;
PI

KW regulatory tissue growth; inhibin; chemostatic; chemokinetic;
 KW haemostatic; thrombolytic; tumour inhibitor; anti-inflammatory;
 XX gene therapy; screening.

OS Homo sapiens.

XX WO9927094-A2.

XX 03-JUN-1999.

XX 20-NOV-1998; 98WO-JP005238.

XX 25-NOV-1997; 97JP-00323129.

XX (SAGA) SAGAMI CHEM RES CENT.

PA (PROT-) PROTEGENE INC.

XX Kato S, Kimura T, Sekine S;

PI WPI; 1999-357835/30.

XX Novel proteins containing transmembrane domains, useful as anti-inflammatory, immune stimulators/suppressors and tissue growth compounds.

XX Disclosure; Page 87-89; 89pp; English.

CC This invention describes novel human transmembrane containing proteins and their encoding nucleic acids. Although no specific use is given for the proteins, they may have a range of activities selected from CC nutritional uses, cytokine and cell differentiation, immune CC stimulation/suppression, haematopoiesis regulatory, tissue growth, CC activin/inhibin, chemostatic/chemokinetic, haemostatic/thrombolytic, CC receptor/ligand, tumour inhibitor, anti-inflammatory and other undefined CC activities. The cDNAs can be utilized as probes for gene diagnosis and as CC gene sources for gene therapy. The cDNAs can also be used for large scale CC expression of proteins. The transformed cells can be used for detection CC of the corresponding ligands and for screening of novel low-molecular CC pharmaceuticals

XX Sequence 383 AA;

Query Match 97.6%; Score 2080; DB 2; Length 383;
 Best Local Similarity 100.0%; Pred. No. 2.8e-147; Indels 0; Gaps 0;
 Matches 383; Conservative 0; Mismatches 0;

QY 1 MAGIPGLLFLPFLCAVGVSPYAPWKPPTWPAAYRPLPVLPQSTLNLAKEPFGAEAKLE 60

DB 1 MAGIPGLLFLPFLCAVGVSPYAPWKPPTWPAAYRPLPVLPQSTLNLAKEPFGAEAKLE 60

QY 61 VSSSCGPOCHKTPLTYEAKQYLSYETLYANGSRTEQVGIYILSSSGDGAQHRDGS 120

DB 61 VSSSCGPOCHKTPLTYEAKQYLSYETLYANGSRTEQVGIYILSSSGDGAQHRDGS 120

QY 121 SGKSRKRQIYGYDSRFSIFGKDFLLNYPFSTSVKLSCTGTGLVAEKHVLTAACHIDG 180

DB 121 SGKSRKRQIYGYDSRFSIFGKDFLLNYPFSTSVKLSCTGTGTGLVAEKHVLTAACHIDG 180

QY 181 KTVYKGTQKLRVGLFKPKFGDGRGANDSTSAPEQMKFQWIRVKRTHVPKGIKGNAND 240

DB 181 KTVYKGTQKLRVGLFKPKFGDGRGANDSTSAPEQMKFQWIRVKRTHVPKGIKGNAND 240

QY 241 IGMDDYALLELKKPKRPFMKIIGVSPAPKQLPGRIHFGSYNDPRLNLYRFDCKDKE 300

DB 241 IGMDDYALLELKKPKRPFMKIIGVSPAPKQLPGRIHFGSYNDPRLNLYRFDCKDKE 300

QY 301 TYDLLYQCDAPGASGSGVYVEMWKQKQKWERKLIIGIFSGHWDNMGSPDENVAVR 360

DB 301 TYDLLYQCDAPGASGSGVYVEMWKQKQKWERKLIIGIFSGHWDNMGSPDENVAVR 360

QY 361 ITPPKYAIQCYWIKGNLYDCREG 383

DB 361 ITPPKYAIQCYWIKGNLYDCREG 383

RESULT 4

AA08657

ID AAY08657 standard; protein; 383 AA.

XX AC AAY08657;

XX DT 09-AUG-1999 (first entry)

XX DE Human transmembrane domain containing protein from clone HP10493.

XX KW Transmembrane domain; human; nutrition; cytokine; cell differentiation;
 KW immune stimulation; immune suppression; haematopoiesis; activin;
 KW regulatory tissue growth; inhibin; chemostatic; chemokinetic;
 KW haemostatic; thrombolytic; tumour inhibitor; anti-inflammatory;
 KW gene therapy; screening.

XX OS Homo sapiens.

XX PN WO9927094-A2.

XX PD 03-JUN-1999.

XX PF 20-NOV-1998; 98WO-JP005238.

XX PR 25-NOV-1997; 97JP-00323129.

XX PA (SAGA) SAGAMI CHEM RES CENT.

XX PA (PROT-) PROTEGENE INC.

XX PI Kato S, Kimura T, Sekine S;

XX WPI; 1999-357835/30.

XX DR N-PSDB; AAX77690, AAX77691.

XX Novel proteins containing transmembrane domains, useful as anti-inflammatory, immune stimulators/suppressors and tissue growth compounds.

XX Claim 1; Page 68-69; 89pp; English.

CC This invention describes novel human transmembrane containing proteins and their encoding nucleic acids. Although no specific use is given for the proteins, they may have a range of activities selected from CC nutritional uses, cytokine and cell differentiation, immune CC stimulation/suppression, haematopoiesis regulatory, tissue growth, CC activin/inhibin, chemostatic/chemokinetic, haemostatic/thrombolytic, CC receptor/ligand, tumour inhibitor, anti-inflammatory and other undefined CC activities. The cDNAs can be utilized as probes for gene diagnosis and as CC gene sources for gene therapy. The cDNAs can also be used for large scale CC expression of proteins. The transformed cells can be used for detection CC of the corresponding ligands and for screening of novel low-molecular CC pharmaceuticals

XX Sequence 383 AA;

Query Match 97.6%; Score 2080; DB 2; Length 383;
 Best Local Similarity 100.0%; Pred. No. 2.8e-147; Indels 0; Gaps 0;
 Matches 383; Conservative 0; Mismatches 0;

QY 1 MAGIPGLLFLPFLCAVGVSPYAPWKPPTWPAAYRPLPVLPQSTLNLAKEPFGAEAKLE 60

DB 1 MAGIPGLLFLPFLCAVGVSPYAPWKPPTWPAAYRPLPVLPQSTLNLAKEPFGAEAKLE 60

QY 61 VSSSCGPOCHKTPLTYEAKQYLSYETLYANGSRTEQVGIYILSSSGDGAQHRDGS 120

DB 61 VSSSCGPOCHKTPLTYEAKQYLSYETLYANGSRTEQVGIYILSSSGDGAQHRDGS 120

QY 121 SGKSRKRQIYGYDSRFSIFGKDFLLNYPFSTSVKLSCTGTGLVAEKHVLTAACHIDG 180

DB 121 SGKSRKRQIYGYDSRFSIFGKDFLLNYPFSTSVKLSCTGTGLVAEKHVLTAACHIDG 180

QY	181	KTYYKGTQKLRVGLFKPKFKDGGRGANDSTSAMPEQMKFQWIRVKRTHVPKGIKGNAND	240
Db	181	KTYYKGTQKLRVGLFKPKFKDGGRGANDSTSAMPEQMKFQWIRVKRTHVPKGIKGNAND	240
QY	241	IGMDYDYLLELKKPKRPMKLGVSPPAKQLPGGRHFSGYDNDPRGNLVYRFCDDVDE	300
Db	241	IGMDYDYLLELKKPKRPMKLGVSPPAKQLPGGRHFSGYDNDPRGNLVYRFCDDVDE	300
QY	301	TYDLLXQQCDAQPGASGSGYVYRMKRRQQQKWERKIIGIFSGHQWDMNGSPQDFNVAVR	360
Db	301	TYDLLXQQCDAQPGASGSGYVYRMKRRQQQKWERKIIGIFSGHQWDMNGSPQDFNVAVR	360
QY	361	ITPLKVAQICYWKIGNYLDREG	383
Db	361	ITPLKVAQICYWKIGNYLDREG	383
RESULT 5			
AAV13390	ID	AAV13390 standard; protein; 383 AA.	
XX	AC	AAV13390;	
XX	XX		
DT	25-JUN-1999	(first entry)	
XX	XX		
DE	XX	Amino acid sequence of protein PRO307.	
XX	XX		
KW	Secreted protein; transmembrane protein; human; enterocolitis;		
KW	Zollinger-Ellison syndrome; gastrointestinal ulceration;		
KW	congenital microvillus atrophy; skin disease; cell growth;		
KW	abnormal keratinocyte differentiation; psoriasis; epithelial cancer;		
KW	Parkinson's disease; Alzheimer's disease; ALS; neuropathy; fibromodulin;		
KW	dermal scarring; Usher Syndrome; Atrophia areata; anti-thrombotic;		
KW	wound healing; tissue repair.		
XX	XX		
OS	Homo sapiens.		
XX	XX		
PN	WO9914328-A2.		
XX	XX		
PD	25-MAR-1999.		
XX	XX		
PF	16-SEP-1998;	98WO-US019330.	
XX	XX		
PR	17-SEP-1997;	97US-0059113P.	
PR	17-SEP-1997;	97US-0059115P.	
PR	17-SEP-1997;	97US-0059117P.	
PR	17-SEP-1997;	97US-0059119P.	
PR	17-SEP-1997;	97US-0059121P.	
PR	17-SEP-1997;	97US-0059122P.	
PR	17-SEP-1997;	97US-0059184P.	
PR	18-SEP-1997;	97US-0059263P.	
PR	18-SEP-1997;	97US-0059266P.	
PR	15-OCT-1997;	97US-0062125P.	
PR	17-OCT-1997;	97US-0062285P.	
PR	17-OCT-1997;	97US-0062287P.	
PR	21-OCT-1997;	97US-0063486P.	
PR	24-OCT-1997;	97US-0062814P.	
PR	24-OCT-1997;	97US-0062816P.	
PR	24-OCT-1997;	97US-0063045P.	
PR	24-OCT-1997;	97US-0063120P.	
PR	24-OCT-1997;	97US-0063121P.	
PR	24-OCT-1997;	97US-0063127P.	
PR	24-OCT-1997;	97US-0063128P.	
PR	27-OCT-1997;	97US-0063327P.	
PR	27-OCT-1997;	97US-0063329P.	
PR	28-OCT-1997;	97US-0063541P.	
PR	28-OCT-1997;	97US-0063542P.	
PR	28-OCT-1997;	97US-0063544P.	
PR	28-OCT-1997;	97US-0063549P.	
PR	28-OCT-1997;	97US-0063550P.	
PR	28-OCT-1997;	97US-0063564P.	
PR	29-OCT-1997;	97US-0063435P.	
PR	29-OCT-1997;	97US-0063704P.	

PR	29-OCT-1997;	97US-0063732P.	
PR	29-OCT-1997;	97US-0063734P.	
PR	29-OCT-1997;	97US-0063735P.	
PR	29-OCT-1997;	97US-0063738P.	
PR	29-OCT-1997;	97US-0064215P.	
PR	31-OCT-1997;	97US-0063870P.	
PR	31-OCT-1997;	97US-0064103P.	
PR	03-NOV-1997;	97US-0064248P.	
PR	07-NOV-1997;	97US-0064809P.	
PR	12-NOV-1997;	97US-0065186P.	
PR	17-NOV-1997;	97US-0065846P.	
PR	18-NOV-1997;	97US-0065693P.	
PR	21-NOV-1997;	97US-0066120P.	
PR	21-NOV-1997;	97US-0066364P.	
PR	24-NOV-1997;	97US-0066453P.	
PR	24-NOV-1997;	97US-0066466P.	
PR	24-NOV-1997;	97US-0066511P.	
PR	24-NOV-1997;	97US-0066770P.	
PR	24-NOV-1997;	97US-0066772P.	
PR	25-NOV-1997;	97US-0066840P.	
XX	XX	(GETH) GENENTECH INC.	
PA	XX		
XX	XX	Wood WI, Gurney AL, Goddard A, Pennica D, Chen J, Yuan J;	
PI	XX		
DR	WPI; 1999-229533/19.		
DR	N-PSDB; AAX52261.		
XX	XX	New isolated human genes and polypeptides used in, e.g. treatment of	
PT	Gastrointestinal ulceration.		
XX	XX	Claim 12; Fig 96; 320pp; English.	
PS	XX	AAV13344-403 represent secreted and transmembrane human proteins. The	
CC	XX	cDNA sequences are obtained from cDNA libraries, prepared from fetal	
CC	XX	lung, fetal kidney, fetal brain, fetal liver and fetal retina. The	
CC	XX	encoded polypeptides have specific uses based on their homology to known	
CC	XX	polypeptides, e.g. PRO211 and PRO217 can be used for disorders associated	
CC	XX	with the preservation and maintenance of gastrointestinal mucosa and the	
CC	XX	repair of acute and chronic mucosal lesions (e.g. enterocolitis,	
CC	XX	Zollinger-Ellison syndrome, gastrointestinal ulceration and congenital	
CC	XX	microvillus atrophy), skin diseases associated with abnormal keratinocyte	
CC	XX	differentiation (e.g. psoriasis, epithelial cancers such as lung squamous	
CC	XX	cell carcinoma of the vulva and gliomas), potent effects on cell growth	
CC	XX	and development, diseases related to growth or survival of nerve cells	
CC	XX	including Parkinson's disease, Alzheimer's disease, ALS, neuropathies or	
CC	XX	cancer. PRO265 can be used as for fibromodulin, e.g. for reducing dermal	
CC	XX	scarring. PRO264 can be used as a target for anti-tumor drugs. PRO533 may	
CC	XX	be used in the treatment of Usher Syndrome or Atrophia areata; PRO269 can	
CC	XX	be used as an anti-thrombotic agent; PRO287 polypeptides and portions may	
CC	XX	have therapeutic applications in wound healing and tissue repair; PRO317	
CC	XX	can be used for treating problems of the kidney, uterus, endometrium,	
CC	XX	blood vessels, or related tissue, e.g. in the heart of genital tract	
XX	XX		
SQ	Sequence 383 AA;		
Query Match			
Best Local Similarity 97.6%; Score 2080; DB 2; Length 383;			
Matches 383; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
QY	1	MAGIFGLLFLFFLLCAVGQVSPYSAPMKPTWPAYRLPVLPQSTLNLAKPDPGAEAKLE	60
Db	1	MAGIFGLLFLFFLLCAVGQVSPYSAPMKPTWPAYRLPVLPQSTLNLAKPDPGAEAKLE	60
QY	61	VSSSCGPOCHKGTPLPTYEAKQYLSYETLYANGSRTETQVGIYILSSSGDGAQHRDGS	120
Db	61	VSSSCGPOCHKGTPLPTYEAKQYLSYETLYANGSRTETQVGIYILSSSGDGAQHRDGS	120
QY	121	SGKSRKRQIYGYDSRFSIFGKDFLLNYPFSTSVKLSGTCTGLVAEKHLVTAACHIDG	180
Db	121	SGKSRKRQIYGYDSRFSIFGKDFLLNYPFSTSVKLSGTCTGLVAEKHLVTAACHIDG	180
QY	181	KTYYKGTQKLRVGLFKPKFKDGGRGANDSTSAMPEQMKFQWIRVKRTHVPKGIKGNAND	240

Db 181 KTVVGTQKLRVGLFKPKFGKGGRGANDSTSAPEQMKFQWIRKRVTHVPKGIKGNAND 240
Qy 241 IGMNDYDYLLELKKPKHKKFMKICVSPPAKQLPGGRHFGSGYDNDPGLNLYRFCVDKDE 300
Db 241 IGMNDYDYLLELKKPKHKKFMKICVSPPAKQLPGGRHFGSGYDNDPGLNLYRFCVDKDE 300
Qy 301 TYDLLYQCDQAQFGASGSGVYVMMKQKQKWERKIIGIFSGHGWYDMNGSPQDFNVAVR 360
Db 301 TYDLLYQCDQAQFGASGSGVYVMMKQKQKWERKIIGIFSGHGWYDMNGSPQDFNVAVR 360
Qy 361 ITELKVAQICYWIKNYLDCCREG 383
Db 361 ITELKVAQICYWIKNYLDCCREG 383

RESULT 6

AAy88277
ID AAY88277 standard; protein; 383 AA.
XX
AC AAY88277;
XX
DT 16-OCT-2000 (first entry)
XX
DE Human TANGO 186 protein.
XX
KW TANGO 180; TANGO 181; TANGO 182; TANGO 183; TANGO 184; TANGO 185;
KW TANGO 186; TANGO 188; TANGO 189; TANGO 215; TANGO 187; human; murine;
KW secreted protein; transmembrane protein; gene therapy; vaccine;
KW diagnosis; treatment; detection.
XX
OS Homo sapiens.
XX
PN WO200018904-A2.
XX
PD 06-APR-2000.
XX
PF 30-SEP-1999; 99WO-US022817.
XX
PR 30-SEP-1998; 98US-00164220.
PR 02-OCT-1998; 98US-00164169.
XX
PA (WILL-) MILLENNIUM BIOTHERAPEUTICS INC.
XX
PI Barnes TW;
XX
DR WPI; 2000-293144/25.
DR N-PSDB; AAA39945, AAA39946.

XX Isolated nucleic acids encoding TANGO polypeptides useful for preventing,
PT diagnosing and treating diseases associated with inappropriate protein
PT expression.
XX
XX Claim 9; Fig 13; 249pp; English.
PS
XX This invention describes novel human and murine nucleic acids encoding
CC TANGO polypeptides (which are either wholly secreted or transmembrane
CC proteins) which can be used for gene therapy and/or vaccination. The
CC peptides are designated TANGO 180 to TANGO 189 and TANGO 215. The nucleic
CC acids may be used to produce TANGO 180 to TANGO 189 and TANGO 215
CC polypeptides according to standard recombinant DNA methodologies. They
CC may also be used to detect and quantify the presence of TANGO nucleic
CC acids in a sample and therefore identify or diagnose diseases associated
CC with inappropriate TANGO expression (e.g. diseases related to over or
CC under expression of the polypeptides or the expression of inactive
CC polypeptides). The nucleic acids and the polypeptides they encode may be
CC used according to standard gene therapy protocols, to treat diseases
CC associated with inappropriate TANGO expression by supplementing a
CC patients own production of the polypeptide of to rectify mutations that
CC may result in expression of an abnormally active polypeptide. The
CC polypeptides may also be used to identify and produce agonists and
CC antagonists of TANGO expression and activity which may be used to
CC modulate TANGO related processes and diseases. The polypeptides are

CC particularly useful for use as antigens for producing antibodies to TANGO
CC proteins which may be used for inhibiting the activity of TANGO proteins.
CC They may also be used to detect and quantify the presence of TANGO
CC proteins in samples and therefore identify patients in whom the protein
CC is over- or under-expressed. This sequence represents the human TANGO 186
CC protein described in the method of the invention
XX

SQ Sequence 383 AA;

Query Match 97.6%; Score 2080; DB 3; Length 383;
Best Local Similarity 100.0%; Pred. No. 2.8e-147;
Matches 383; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MAGIPGLLFLFLCAVGVSPYAPWKPWPAYRLPVVLPQSTLNLAKEPFGAIAKLE 60
Db 1 MAGIPGLLFLFLCAVGVSPYAPWKPWPAYRLPVVLPQSTLNLAKEPFGAIAKLE 60
Qy 61 VSSSCGPQCHKTPLTPTVEEAKQYLSYETLYANGSRTEQVGIYIILSSGDAQHRDGS 120
Db 61 VSSSCGPQCHKTPLTPTVEEAKQYLSYETLYANGSRTEQVGIYIILSSGDAQHRDGS 120
Qy 121 SGKSRKROIYGYDSRFSIFGKDFLLNYPFSTSVKLSCTGTGLVAEKHVLTAACIHGD 180
Db 121 SGKSRKROIYGYDSRFSIFGKDFLLNYPFSTSVKLSCTGTGLVAEKHVLTAACIHGD 180
Qy 181 KTVVGTQKLRVGLFKPKFGKGGRGANDSTSAPEQMKFQWIRKRVTHVPKGIKGNAND 240
Db 181 KTVVGTQKLRVGLFKPKFGKGGRGANDSTSAPEQMKFQWIRKRVTHVPKGIKGNAND 240
Qy 241 IGMNDYDYLLELKKPKHKKFMKIGVSPPAKQLPGGRHFGSGYDNDPGLNLYRFCVDKDE 300
Db 241 IGMNDYDYLLELKKPKHKKFMKIGVSPPAKQLPGGRHFGSGYDNDPGLNLYRFCVDKDE 300
Qy 301 TYDLLYQCDQAQFGASGSGVYVMMKQKQKWERKIIGIFSGHGWYDMNGSPQDFNVAVR 360
Db 301 TYDLLYQCDQAQFGASGSGVYVMMKQKQKWERKIIGIFSGHGWYDMNGSPQDFNVAVR 360
Qy 361 ITELKVAQICYWIKNYLDCCREG 383
Db 361 ITELKVAQICYWIKNYLDCCREG 383

RESULT 7

AAy87270
ID AAY87270 standard; protein; 383 AA.
XX
AC AAY87270;
XX
DT 11-MAY-2000 (first entry)
XX
DE Human signal peptide containing protein HSPP-47 SEQ ID NO:47.
XX
KW Human; signal peptide-containing protein; HSPP; diagnosis; cancer;
KW inflammation; cardiovascular disease; anticancer; anti-inflammatory;
KW antimicrobial; nootropic; neuroprotective; cardiovascular; hepatotropic;
KW antiasthmatic; gene therapy; cell proliferation; neurological disorder;
KW reproductive disorder; developmental disorder; arteriosclerosis;
KW cirrhosis; psoriasis; acquired immune deficiency syndrome; anaemia;
KW asthma; Crohn's disease; infection; Alzheimer's disease; schizophrenia;
KW Parkinson's disease; Huntington's disease; ovulatory defect;
KW muscular dystrophy.
OS Homo sapiens.
XX
XX WO200000610-A2.
XX
PD 06-JAN-2000.
XX
PF 25-JUN-1999; 99WO-US014484.
XX
PR 26-JUN-1998; 98US-0090762P.
PR 31-JUL-1998; 98US-0094983P.
PR 01-OCT-1998; 98US-0102686P.

PR	11-DEC-1998;	98US-0112129P.	
XX	(INCY-) INCYTE PHARM INC.		
XX	Lal P, Tang YT, Gorgone GA, Corley NC, Guegler KJ, Baughn ME;		
PI	Akerblom IE, Au-Young J, Yue H, Patterson C, Reddy R, Hillman JL;		
PI	Bandman O;		
XX	WPI; 2000-160673/14.		
DR	N-PSDB; AA298155.		
XX	New human signal peptide-containing proteins useful in treatment,		
PT	prevention and diagnosis of e.g. cancer, inflammation and cardiovascular		
PT	disease.		
XX	Claim 1; Page 192-193; 327pp; English.		
XX	AAZ98109 to AAZ98242 encode AAY87224 to AAY87357 which represent the		
CC	human signal peptide-containing proteins HSP-1 to HSP-134. HSPs have		
CC	anticancer, anti-inflammatory, antimicrobial, nootropic, hepatotropic,		
CC	neuroprotective, cardiovascular and antiasthmatic activities, and can be		
CC	used in gene therapy. HSPs can be used to treat or prevent disorders		
CC	associated with decreased activity or function of HSP. Antagonists of		
CC	HSP are used to treat or prevent disorders associated with increased		
CC	activity or function of HSP. Such diseases include cell proliferation		
CC	(including cancer), inflammation, cardiovascular, neurological,		
CC	reproductive or developmental disorders, (e.g. arteriosclerosis,		
CC	cirrhosis, psoriasis, acquired immune deficiency syndrome, congestive or		
CC	asthma, Crohn's disease, microbial or other infections, congestive or		
CC	ischaemic heart disease, Alzheimer's, Parkinson's or Huntington's		
CC	diseases, schizophrenia, ovulatory defects, muscular dystrophy). HSP		
CC	nucleic acids can be used for the recombinant production of HSP, for		
CC	detecting HSP in standard hybridisation and amplification assays (for		
CC	diagnosis and monitoring), in gene therapy, as antisense, triplex-forming		
CC	or ribozyme therapeutics, for detecting related sequences or genetic		
CC	variations, and for chromosomal mapping. HSP are also used to raise		
CC	specific antibodies (Ab) and to screen for agonists and antagonists		
CC	(potential therapeutic agents). Ab are used to diagnose, or monitor, HSP		
CC	-related diseases (in usual immunoassays), as therapeutic antagonists, in		
CC	competitive drug screens, and for purification of HSP from natural		
CC	sources		
XX	Sequence 383 AA;		
SQ			
Query Match 97.6%; Score 2080; DB 3; Length 383;			
Best Local Similarity 100.0%; Pred. No. 2,8e-147;			
Matches 383; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
QY	1	MAGIPGLLFLFLCAVGVSPYSAPWKPTWPAYRLPVVLPGSTLNLAKPFGAEAKLE	60
Db	1	MAGIPGLLFLFLCAVGVSPYSAPWKPTWPAYRLPVVLPGSTLNLAKPFGAEAKLE	60
QY	61	VSSSCGQCHKTPLTYEAKQYLSYETLYANGSTETQVGIYILSSGCGAQRHDSGS	120
Db	61	VSSSCGQCHKTPLTYEAKQYLSYETLYANGSTETQVGIYILSSGCGAQRHDSGS	120
QY	121	SGKSRKRQIYGVDSRFSIFGKDFLNLNYPFSTSVKLSLSTGCTGLVAEKHVLTAACHIDG	180
Db	121	SGKSRKRQIYGVDSRFSIFGKDFLNLNYPFSTSVKLSLSTGCTGLVAEKHVLTAACHIDG	180
QY	181	KTYVGTQKLRVFLKPKFKDGGGRANDSTSAMPEQMKFQWIRVVRKTHVPKGMIGNAND	240
Db	181	KTYVGTQKLRVFLKPKFKDGGGRANDSTSAMPEQMKFQWIRVVRKTHVPKGMIGNAND	240
QY	241	IGWDYDYLLELKKPKHKKFMKIGVSPPAKOLPGGRHIFSGVNDNPGNLVRFCDVKDE	300
Db	241	IGWDYDYLLELKKPKHKKFMKIGVSPPAKOLPGGRHIFSGVNDNPGNLVRFCDVKDE	300
QY	301	TYDLLYQQCDAOPGASGSGVYVVMWKRQQQKWERKLIIGIFSGHQWDMNGSPQDFNVAVR	360
Db	301	TYDLLYQQCDAOPGASGSGVYVVMWKRQQQKWERKLIIGIFSGHQWDMNGSPQDFNVAVR	360
QY	361	ITPLKYAQICYWIKGNLYDCREG 383	

Db	361	ITPLKYAQICYWIKGNLYDCREG 383	
RESULT 8			
AAZ53627			
ID	AAZ53627	standard; protein; 383 AA.	
XX	AAZ53627;		
XX	22-FEB-2000	(first entry)	
DE	A bone marrow secreted protein designated BMS192.		
XX	Bone marrow secreted protein; bone marrow stromal cell; cytokine;		
KW	cell proliferation; cell differentiation; hematopoiesis; anaemia;		
KW	myeloid cell deficiency; lymphoid cell deficiency; myeloid cell;		
KW	erythroid progenitor cell; colony stimulating factor; granulocyte;		
KW	monocyte; macrophage; myelo-suppression; megakaryocyte; platelet;		
KW	platelet disorder; thrombocytopenia; hematopoietic stem cell;		
KW	stem cell disorder; aplastic anaemia; bone differentiation;		
KW	paroxysmal nocturnal hemoglobinuria; bone growth; cartilage; tendon;		
KW	ligament; nerve; wound healing; tissue repair; burn; incision; ulcer;		
KW	bone fracture; cartilage damage; artificial joint.		
XX	Homo sapiens.		
OS			
XX	Key	Location/Qualifiers	
FT	Peptide	1..19	
FT		/note= "signal peptide"	
XX	W099333979-A2.		
XX	08-JUL-1999.		
XX	18-DEC-1998;	98WO-US027008.	
XX	30-DEC-1997;	97US-0068958P.	
PR	24-SEP-1998;	98US-0101603P.	
PR	30-SEP-1998;	98US-0102540P.	
XX	(CHIR) CHIRON CORP.		
XX	Lin H, Cao L;		
XX	WPI: 2000-038344/03.		
DR	N-PSDB; AAZ36233.		
XX	New isolated human polynucleotide and secreted proteins can induce		
PT	production of other cytokines in certain cell populations.		
XX	Claim 2; Page 81-82; 120pp; English.		
XX	AAZ53622-43 represent bone marrow secreted proteins of human bone marrow		
CC	stromal cells. The proteins can exhibit cytokine, cell proliferation, or		
CC	cell differentiation activity (either inducing or inhibiting). They can		
CC	be used to support colony forming cells or factor-dependent cell lines,		
CC	to regulate hematopoiesis, and to treat myeloid or lymphoid cell		
CC	deficiencies. In addition, they may be used to support the growth and		
CC	proliferation of erythroid progenitor cells, and to treat various		
CC	anaemias. They can have colony stimulating factor (CSF) activity and can		
CC	be used to support the growth and proliferation of myeloid cells such as		
CC	granulocytes, monocytes or macrophages, to prevent or treat myelo-		
CC	suppression, to support the growth and proliferation of megakaryocytes		
CC	and platelets, thereby allowing prevention or treatment of platelet		
CC	disorders such as thrombocytopenia, to support the growth and		
CC	proliferation of hematopoietic stem cells, either in place of or in		
CC	conjunction with platelet transfusions, to treat stem cell disorders,		
CC	such as aplastic anaemia and paroxysmal nocturnal hemoglobinuria, or to		
CC	repopulate the stem cell compartment after irradiation or chemotherapy.		
CC	They can be used for growth or differentiation of bone, cartilage, and		
CC	tendon, ligament, or nerve tissue, as well as for wound healing and		
CC	tissue repair and replacement, and in the treatment of burns, incisions		

CC and ulcers, to induce cartilage and/or bone growth in circumstances where
CC bone is not normally formed and thus have an application in healing bone
CC fractures and cartilage damage or defects, prophylactic use in fracture
CC reduction and also in the improved fixation of artificial joints
XX
SQ Sequence 383 AA;

Query Match 97.6%; Score 2080; DB 3; Length 383;
Best Local Similarity 100.0%; Pred. No. 2.8e-147;
Matches 383; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAGIPGLLFLFLCAVGVSPYSAPWKPWPAYRLPVVLPQSTLNLAKEPFGAEAKLE 60
DB 1 MAGIPGLLFLFLCAVGVSPYSAPWKPWPAYRLPVVLPQSTLNLAKEPFGAEAKLE 60
QY 61 VSSSCGPOCHKGTPLTYEAKQYLSYETLYANGSRTEQVGIYILSSSGDGAQHRDGS 120
DB 61 VSSSCGPOCHKGTPLTYEAKQYLSYETLYANGSRTEQVGIYILSSSGDGAQHRDGS 120
QY 121 SGKRRKROIYGYDSRFSIFGKDFLLNYPFSTSVKLSGTCTGLVAEKHVLTAACHIDG 180
DB 121 SGKRRKROIYGYDSRFSIFGKDFLLNYPFSTSVKLSGTCTGLVAEKHVLTAACHIDG 180
QY 181 KTYVGTQKLRVGLFKPKFKDGGGANDSTSAMPEQMKFQWIRVKRTHVPKGIKNAND 240
DB 181 KTYVGTQKLRVGLFKPKFKDGGGANDSTSAMPEQMKFQWIRVKRTHVPKGIKNAND 240
QY 241 IGMVDYALLELKKPHKRFKMGKIVGSPPAKQLPGGRHPSGYNDNRPGNLVRFCDVDE 300
DB 241 IGMVDYALLELKKPHKRFKMGKIVGSPPAKQLPGGRHPSGYNDNRPGNLVRFCDVDE 300
QY 301 TYDLLYQCCDAQPGASGSGVYVRMKRQKQKWERKLIIGIFSGHWDVMDNGSPQDFNVAVR 360
DB 301 TYDLLYQCCDAQPGASGSGVYVRMKRQKQKWERKLIIGIFSGHWDVMDNGSPQDFNVAVR 360
QY 361 ITPLKYAQICYWIKGNLYDCREG 383
DB 361 ITPLKYAQICYWIKGNLYDCREG 383

RESULT 9
AAB25618
ID AAB25618 standard; protein; 383 AA.

AC AAB25618;

DT 21-NOV-2000 (first entry)

DE Protein encoded by human secreted protein gene #10.

XX Secreted protein; immunosuppressant; anti-inflammatory; antiarthritic;
KW antirheumatic; dermatological; antiproliferative; antiarteriosclerotic;
KW anticancer; vulnary; antiviral; antibacterial; antifungal;
KW immune disorder; Addison's disease; rheumatoid arthritis; dermatitis;
KW multiple sclerosis; inflammatory disorder; inflammatory bowel disease;
KW Crohn's disease; nephritis; hyperproliferative disorder;
KW cardiovascular disorder; coronary arteriosclerosis; myocarditis; cancer;
KW melanoma; lymphoma; wound healing; human; chromosome 12.

OS Homo sapiens.

XX WO200029435-A1.

XX 25-MAY-2000.

XX 27-OCT-1999; 99WO-US025031.

XX 28-OCT-1998; 98US-0105971P.

XX (HUMA-) HUMAN GENOME SCI INC.

XX Ni J, Ruben SM, Olsen HS, Young PE, Kenny JJ, Moore PA, Wei Y;
PI Greene JM;

XX WPI; 2000-387742/33.

XX Isolated nucleic acid molecules encoding human secreted proteins are used
PT for the prevention, amelioration and treatment of autoimmune,
PT inflammatory, hyperproliferative and cardiovascular disorders, cancer,
PT wounds, and infectious diseases.

XX Disclosure; Page 169; 803pp; English.

XX The present invention relates to 12 secreted human proteins and the
CC nucleotide sequences encoding them. The polynucleotide sequences given in
CC AAB0606-A80623 encode the 12 secreted protein sequences given in
CC AAB25576-B25593. The human secreted proteins have various activities
CC dependent on the tissues in which they are expressed. Examples of the
CC activities of the proteins include: immunosuppressant; anti-inflammatory;
CC antirheumatic; antirheumatic; dermatological; antiproliferative;
CC antiarteriosclerotic; anticancer; vulnary; antiviral; antibacterial;
CC and antifungal activity. The proteins, polypeptides, agonists and
CC antagonists may be used to treat prevent and/or diagnose various disease,
CC disorders and conditions examples of which include: immune disorders e.g.
CC Addison's disease, rheumatoid arthritis, dermatitis, and multiple
CC sclerosis; inflammatory disorders e.g. inflammatory bowel disease,
CC Crohn's disease and nephritis; hyperproliferative disorders such as
CC paraproteinemia and purpura; cardiovascular disorders e.g. coronary
CC arteriosclerosis and myocarditis; cancer e.g. melanoma and lymphoma.
CC The proteins and polynucleotide sequences may also be used in wound healing
CC and the treatment of infectious diseases. The human secreted protein gene
CC #10 and protein sequences are represented in sequences AAB0615 and
CC AAB25585. Secreted protein gene #10 is located on chromosome 12.
CC Sequences AAB25616-B25618 represent alternative secreted protein #10
CC sequences and AAB06629-A80676 represent genes which are related to the
CC secreted protein gene#10

XX Sequence 383 AA;

Query Match 97.6%; Score 2080; DB 3; Length 383;

Best Local Similarity 100.0%; Pred. No. 2.8e-147;
Matches 383; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAGIPGLLFLFLCAVGVSPYSAPWKPWPAYRLPVVLPQSTLNLAKEPFGAEAKLE 60

DB 1 MAGIPGLLFLFLCAVGVSPYSAPWKPWPAYRLPVVLPQSTLNLAKEPFGAEAKLE 60

QY 61 VSSSCGPOCHKGTPLTYEAKQYLSYETLYANGSRTEQVGIYILSSSGDGAQHRDGS 120

DB 61 VSSSCGPOCHKGTPLTYEAKQYLSYETLYANGSRTEQVGIYILSSSGDGAQHRDGS 120

QY 121 SGKRRKROIYGYDSRFSIFGKDFLLNYPFSTSVKLSGTCTGLVAEKHVLTAACHIDG 180

DB 121 SGKRRKROIYGYDSRFSIFGKDFLLNYPFSTSVKLSGTCTGLVAEKHVLTAACHIDG 180

QY 181 KTYVGTQKLRVGLFKPKFKDGGGANDSTSAMPEQMKFQWIRVKRTHVPKGIKNAND 240

DB 181 KTYVGTQKLRVGLFKPKFKDGGGANDSTSAMPEQMKFQWIRVKRTHVPKGIKNAND 240

QY 241 IGMVDYALLELKKPHKRFKMGKIVGSPPAKQLPGGRHPSGYNDNRPGNLVRFCDVDE 300

DB 241 IGMVDYALLELKKPHKRFKMGKIVGSPPAKQLPGGRHPSGYNDNRPGNLVRFCDVDE 300

QY 301 TYDLLYQCCDAQPGASGSGVYVRMKRQKQKWERKLIIGIFSGHWDVMDNGSPQDFNVAVR 360

DB 301 TYDLLYQCCDAQPGASGSGVYVRMKRQKQKWERKLIIGIFSGHWDVMDNGSPQDFNVAVR 360

QY 361 ITPLKYAQICYWIKGNLYDCREG 383

DB 361 ITPLKYAQICYWIKGNLYDCREG 383

RESULT 10

AAB25592

ID AAB25592 standard; protein; 383 AA.

XX

AC AAB25592;
 XX 21-NOV-2000 (first entry)
 XX
 DE Protein encoded by human secreted protein gene #10 clone HUSQ05.
 XX
 KW Secreted protein; immunosuppressant; anti-inflammatory; antiarthritic;
 KW antihemetic, dermatological; antiproliferative; antiarthritic;
 KW anticancer; vulnary; antiviral; antibacterial; antifungal;
 KW immune disorder; Addison's disease; rheumatoid arthritis; dermatitis;
 KW multiple sclerosis; inflammatory disorder; inflammatory bowel disease;
 KW Crohn's disease; nephritis; hyperproliferative disorder;
 KW cardiovascular disorder; coronary arteriosclerosis; myocarditis; cancer;
 KW melanoma; lymphoma; wound healing; human; chromosome 12.
 XX
 OS Homo sapiens.
 XX
 XX WO200029435-A1.
 PN
 XX
 XX 25-MAY-2000.
 PD
 XX 27-OCT-1999; 99WO-US025031.
 PF
 XX 28-OCT-1998; 98US-0105971P.
 PR
 XX (HUMA-) HUMAN GENOME SCI INC.
 PA
 XX Ni J, Ruben SM, Olsen HS, Young PE, Kenny JJ, Moore PA, Wei Y;
 PI Greene JM;
 XX
 XX WPI; 2000-387742/33.
 XX
 XX Isolated nucleic acid molecules encoding human secreted proteins are used
 XX for the prevention, amelioration and treatment of autoimmune,
 XX inflammatory, hyperproliferative and cardiovascular disorders, cancer,
 XX wounds, and infectious diseases.
 XX
 PS Claim 1; Page 684-685; 803pp; English.
 XX
 CC The present invention relates to 12 secreted human proteins and the
 CC nucleotide sequences encoding them. The polynucleotide sequences given in
 CC AAB0606-A060623 encode the 12 secreted protein sequences given in
 CC AAB2576-B25593. The human secreted proteins have various activities
 CC dependent on the tissues in which they are expressed. Examples of the
 CC activities of the proteins include: immunosuppressant; anti-inflammatory;
 CC antiarthritic; antirheumatic, dermatological; antiproliferative;
 CC antiarteriosclerotic; anticancer; vulnary; antiviral; antibacterial;
 CC and antifungal activity. The proteins, polypeptides, agonists and
 CC antagonists may be used to treat prevent and/or diagnose various disease,
 CC disorders and conditions examples of which include: immune disorders e.g.
 CC Addison's disease, rheumatoid arthritis, dermatitis, and multiple
 CC sclerosis; inflammatory disorders e.g. inflammatory bowel disease,
 CC Crohn's disease and nephritis; hyperproliferative disorders such as
 CC paraproteinemia and purpura; cardiovascular disorders e.g. coronary
 CC arteriosclerosis and myocarditis; cancer e.g. melanoma and lymphoma. The
 CC proteins and polynucleotide sequences may also be used in wound healing
 CC and the treatment of infectious diseases. The human secreted protein gene
 CC #10 and protein sequences are represented in sequences AAB0615 and
 CC AAB25585. Secreted protein gene #10 is located on chromosome 12.
 CC Sequences AAB25618-B25618 represent alternative secreted protein #10
 CC sequences and AAB0669-A06076 represent genes which are related to the
 CC secreted protein gene#10
 XX
 SQ Sequence 383 AA;

Query Match 97.6%; Score 2080; DB 3; Length 383;

Best Local Similarity 100.0%; Pred. No. 2.8e-147;

Matches 383; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAGIPGLFLLFLLCAVGVSPYAPWKTWPAYRLPVVLPQSTLNIAKPDFGAEKLE 60

DB 1 MAGIPGLFLLFLLCAVGVSPYAPWKTWPAYRLPVVLPQSTLNIAKPDFGAEKLE 60

QY 61 VSSCGPQCHKGTPLPTVEEAKQYLSYETLYANGRTETQVGIIYILSSSGDGAQHRS DGS 120
 DB |||||
 QY 121 SKSRRKQIYGYDSRFSIFGKDFLLNYPFSTSVKLSGCTGLVAEKHVLTAACHIDG 180
 DB |||||
 QY 181 KTYVKGTKLRVGLFKPKFKDCGGRGANDSTAMPQMKFQWIRVVKRTHVPKGIKGNAND 240
 DB |||||
 QY 241 IGMDYDVALLELKPHKFKFMKIGVSPPAKQLPGGRIHFSGHVDNDRPGLNVRFCVDKDE 300
 DB |||||
 QY 301 TYDLLYQCCDAOPGASGGVYVMWKRQOQKWERKIIGIFSGHQWVDMNGSPQDENVAVR 360
 DB |||||
 QY 361 ITPLKYAQICYWIKGNLYLDCREG 383
 DB |||||
 DB 361 ITPLKYAQICYWIKGNLYLDCREG 383
 RESULT 11
 ADC78573
 ID ADC78573 standard; protein; 383 AA.
 XX
 AC ADC78573;
 XX
 DT 01-JAN-2004 (first entry)
 DE Human PRO307 protein.
 XX
 KW antinflammatory; antiulcer; cytostatic; antipsoriatic; antiparkinsonian;
 KW neurotrophic; neuroprotective; vasotropic; chemotactic; angiogenic;
 KW neurotrophic; osteopathic; antiasthmatic; antiarthritic; antirheumatic;
 KW antiarteriosclerotic; cardiac; antidiabetic; cerebroprotective;
 KW thrombolytic; immunomodulator; enterocolitis; Zollinger-Ellison syndrome;
 KW gastrointestinal ulceration; psoriasis; cancer; Parkinson's disease;
 KW Alzheimer's; ALS; neuropathy; dermal scarring; wound healing;
 KW nerve repair; thrombosis; bone; cartilage formation; angiogenesis;
 KW asthma; rheumatoid arthritis; multiple sclerosis; inflammatory disorder;
 KW atherosclerosis; cardiac injury; infertility; premature aging; AIDS;
 KW diabetes; stroke; gene therapy; transgenic; PRO; human.
 XX
 OS Homo sapiens.
 XX
 WO200015796-A2.
 PD 23-MAR-2000.
 PF 15-SEP-1999; 99WO-US021090.
 PR 16-SEP-1998; 98WO-US019330.
 XX (GETH) GENENTECH INC.
 PA
 XX Chen J, Goddard A, Gurney AL, Hillan K, Pennica D, Wood WI;
 PI Yuan J;
 XX
 XX WPI; 2000-271434/23.
 DR N-PSDB; ADC78572.
 XX
 PT Novel nucleic acids encoding secreted and transmembrane polypeptides with
 PT homology, e.g. to growth and cancer-associated antigens.
 XX
 PS Claim 12; SEQ ID NO 261; 355pp; English.
 XX
 CC The invention relates to a novel nucleic acid encoding a PRO polypeptide.
 CC The polypeptides and polynucleotides of the invention may be useful as
 CC research tools and as therapeutics for treating enterocolitis, Zollinger-

CC Ellison syndrome, gastrointestinal ulceration, psoriasis, cancer,
CC Parkinson's disease, Alzheimer's disease, ALS, neuropathies, dermal
CC scarring and wound healing, nerve repair, thrombosis, bone and/or
CC cartilage formation, angiogenesis, asthma, rheumatoid arthritis, multiple
CC sclerosis, inflammatory disorders, atherosclerosis, cardiac injury,
CC infertility, premature aging, AIDS, diabetes complications and stroke.
CC The molecules may also be utilised during gene therapy procedures and
CC transgenic animal production. The current sequence is that of the human
CC PRO protein of the invention.
XX
SQ Sequence 383 AA;
Query Match 97.6%; Score 2080; DB 3; Length 383;
Best Local Similarity 100.0%; Pred. No. 2.8e-147;
Matches 383; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MAGIPGLLFLFLLCVAVGQVSPYSAPWKPTWPAYRLPVVLPSTLNLAKEPFGAEAKLE 60
DB 1 MAGIPGLLFLFLLCVAVGQVSPYSAPWKPTWPAYRLPVVLPSTLNLAKEPFGAEAKLE 60
QY 61 VSSSCGPOCHKGTPLPTYEAKQYLSYETLYANGSRTETQVGIYILSSGGAQHRDGS 120
DB 61 VSSSCGPOCHKGTPLPTYEAKQYLSYETLYANGSRTETQVGIYILSSGGAQHRDGS 120
QY 121 SGKSRKRQIYGYDSRFSIFGKDFLLNYPFSTSVKLSGTCTGLVAEKHVLTAACHIDG 180
DB 121 SGKSRKRQIYGYDSRFSIFGKDFLLNYPFSTSVKLSGTCTGLVAEKHVLTAACHIDG 180
QY 181 KTYVKGTKLVRGFLKPKFQKGGGRGANDSTSAMPEQMKFQIRVXKTHVPKGIKGNAND 240
DB 181 KTYVKGTKLVRGFLKPKFQKGGGRGANDSTSAMPEQMKFQIRVXKTHVPKGIKGNAND 240
QY 241 IGMVDYALLELKKPHKRFKMGKIGVSPAPKQIPGRIHFSGYNDNDRPGLNLYRFDCKVDE 300
DB 241 IGMVDYALLELKKPHKRFKMGKIGVSPAPKQIPGRIHFSGYNDNDRPGLNLYRFDCKVDE 300
QY 301 TYDLLYQCCDAQPGASGVVYVMWKQKQKWKRIIGIFSGHWDVMDNGSPQDENVAVR 360
DB 301 TYDLLYQCCDAQPGASGVVYVMWKQKQKWKRIIGIFSGHWDVMDNGSPQDENVAVR 360
QY 361 ITPKVAQICWIKGNVLDREG 383
DB 361 ITPKVAQICWIKGNVLDREG 383
RESULT 12
ID AAB80258
XX AAB80258 standard; protein; 383 AA.
AC AAB80258;
XX
DT 24-APR-2001 (first entry)
DE Human PRO307 protein.
XX
KW Human; PRO; dermatological; antipsoriatic; cytostatic; antiinflammatory;
KW antiparkinsonian neurotropic; neuroprotective; vulnerary; cardiac;
KW antiangiogenic; vasotropic; antiasthmatic; antirheumatic; cancer;
KW antithratic; antinfertility; antidiabetic; antiviral; diabetes;
KW ophthalmological; gene therapy; skin disease; gastrointestinal disorder;
KW ischaemia; inflammation.
XX
OS Homo sapiens.
XX
PN WO200104311-A1.
XX
PD 18-JAN-2001.
XX
PF 22-FEB-2000; 2000WO-US0004414.
XX
PR 07-JUL-1999; 99US-0143048P.
PR 26-JUL-1999; 99US-0145698P.
PR 28-JUL-1999; 99US-0146222P.

PR 08-SEP-1999; 99WO-US020594.
PR 13-SEP-1999; 99WO-US020944.
PR 15-SEP-1999; 99WO-US021090.
PR 15-SEP-1999; 99WO-US021547.
PR 05-OCT-1999; 99WO-US023089.
PR 29-NOV-1999; 99WO-US028214.
PR 30-NOV-1999; 99WO-US028313.
PR 02-DEC-1999; 99WO-US028564.
PR 02-DEC-1999; 99WO-US028565.
PR 16-DEC-1999; 99WO-US030095.
PR 20-DEC-1999; 99WO-US030911.
PR 20-DEC-1999; 99WO-US030999.
PR 05-JAN-2000; 2000WO-US000219.
XX
XX (GETH) GENENTECH INC.
XX
PI Ashkenazi AJ, Botstein D, Deenoyers L, Eaton DL, Ferrara N;
PI Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME, Goddard A;
PI Godowski PJ, Grimaldi CJ, Gurney AL, Hillan KJ, Kljavin IJ;
PI Mather JP, Pan J, Paoni NF, Roy MA, Stewart TA, Tumas D;
PI Williams PM, Wood WI;
XX
DR WPI; 2001-081051/09.
DR N-PSDB; AAF72419.
XX
XX Sixty one nucleic acids encoding PRO polypeptides which are useful in the
XX treatment of skin diseases (e.g. psoriasis), cancers (e.g. lung squamous
XX cell carcinoma) and neurodegenerative diseases (e.g. Alzheimer's
XX disease).
PS Claim 1; Fig 96; 393pp; English.
XX
XX The present sequence is one of sixty one novel secreted and transmembrane
XX PRO polypeptides. The PRO polypeptides are useful for treating skin
XX diseases (e.g. psoriasis), cancers (e.g. lung squamous cell carcinoma),
XX gastrointestinal disorders (e.g. enterocolitis), neurodegenerative
XX diseases (e.g. Alzheimer's disease, Parkinson's disease), wound repair,
XX cardiovascular disorders (e.g. endometrial bleeding angiogenesis,
XX ischaemia such as coronary ischaemia, atherosclerosis), inflammatory
XX disorders (e.g. asthma, rheumatoid arthritis, multiple sclerosis),
XX infertility, AIDS and diabetes and retinal disorders such as retinitis
XX pigmentosum. The PRO nucleic acids have applications in molecular
XX biology, including use as hybridization probes, and in chromosome and
XX gene mapping
XX
SQ Sequence 383 AA;
Query Match 97.6%; Score 2080; DB 4; Length 383;
Best Local Similarity 100.0%; Pred. No. 2.8e-147;
Matches 383; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MAGIPGLLFLFLLCVAVGQVSPYSAPWKPTWPAYRLPVVLPSTLNLAKEPFGAEAKLE 60
DB 1 MAGIPGLLFLFLLCVAVGQVSPYSAPWKPTWPAYRLPVVLPSTLNLAKEPFGAEAKLE 60
QY 61 VSSSCGPOCHKGTPLPTYEAKQYLSYETLYANGSRTETQVGIYILSSGGAQHRDGS 120
DB 61 VSSSCGPOCHKGTPLPTYEAKQYLSYETLYANGSRTETQVGIYILSSGGAQHRDGS 120
QY 121 SGKSRKRQIYGYDSRFSIFGKDFLLNYPFSTSVKLSGTCTGLVAEKHVLTAACHIDG 180
DB 121 SGKSRKRQIYGYDSRFSIFGKDFLLNYPFSTSVKLSGTCTGLVAEKHVLTAACHIDG 180
QY 181 KTYVKGTKLVRGFLKPKFQKGGGRGANDSTSAMPEQMKFQIRVXKTHVPKGIKGNAND 240
DB 181 KTYVKGTKLVRGFLKPKFQKGGGRGANDSTSAMPEQMKFQIRVXKTHVPKGIKGNAND 240
QY 241 IGMVDYALLELKKPHKRFKMGKIGVSPAPKQIPGRIHFSGYNDNDRPGLNLYRFDCKVDE 300
DB 241 IGMVDYALLELKKPHKRFKMGKIGVSPAPKQIPGRIHFSGYNDNDRPGLNLYRFDCKVDE 300
QY 301 TYDLLYQCCDAQPGASGVVYVMWKQKQKWKRIIGIFSGHWDVMDNGSPQDENVAVR 360

Db 301 TYDLLYQQCDAQPGASGSGVYVVMKRRQQQKWERKLIIGIFSGHQWDMNGSPQDFNVAVR 360

QY 361 ITPLKYAQICYWIKGNLYDCREG 383

Db 361 ITPLKYAQICYWIKGNLYDCREG 383

RESULT 13

AA848974

ID AA848974 standard; protein; 383 AA.

AC AA848974;

XX 27-MAR-2001 (first entry)

XX Human Zsig13 variant #3, SEQ ID NO:18.

DE Human Zsig13; serine protease; chromosome 11q22.1; elastase homologue;

KW glutamyl endopeptidase homologue; factor X homologue; trypsin homologue;

KW trypsinogen homologue; mast cell protease homologue;

KW collagenase homologue; protein degradation; food processing; brewing;

XX alcohol production; laundry detergent component.

OS Homo sapiens.

XX US6153420-A.

XX 28-NOV-2000.

XX 04-MAY-1998; 98US-00072384.

XX 24-APR-1997; 97US-0044185P.

XX 17-APR-1998; 98US-00062142.

XX (ZYMO) ZYMOGENETICS INC.

XX Sheppard PO;

XX WPI; 2001-060090/07.

XX N-PSDB; AAC91784.

XX New isolated serine protease (designated Zsig13), useful in industrial

PT processes to degrade unwanted proteins or alter the characteristics of

PT protein-containing composition, as well as in industrial applications

PT (e.g. brewing).

XX Claim 1; Col 41-44; 26pp; English.

XX The invention relates to human Zsig13 proteins (AAB48972-B48974), and to

CC DNA encoding them (AAC91782-C91784). The invention also relates to

CC expression vectors and host cells comprising a human Zsig13 DNA, and the

CC recombinant production of a human Zsig13 protein or its precursor. Zsig13

CC is a serine protease, and has significant homology to Bacillus

CC licheniformis glutamyl endopeptidase, human clotting factor X, human

CC elastase, rat mast cell protease, Streptomyces griseus trypsin, bovine

CC trypsinogen, and Hypoderma lineatum collagenase. The gene encoding human

CC Zsig13 is located on chromosome 11q22.1. Zsig13 is useful in industrial

CC processes to degrade unwanted proteins or alter the characteristics of

CC protein-containing compositions. It may also be used in industrial

CC applications in which proteases are utilised, including food processing,

CC brewing and alcohol production, and as a component of a laundry

CC detergent. The present sequence represents a human Zsig13 variant

XX Sequence 383 AA;

SQ

Query Match 97.6%; Score 2080; DB 4; Length 383;

Best Local Similarity 100.0%; Pred. No. 2.8e-147;

Matches 383; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAGIPGLLFLLFLLCAVGVSPYSAPWKTWPAYRLPVVLPQSTLNLAKEPFGAEAKLE 60

Db 1 MAGIPGLLFLLFLLCAVGVSPYSAPWKTWPAYRLPVVLPQSTLNLAKEPFGAEAKLE 60

QY 61 VSSSCGPOCHKGTPLPTVEEAKQYLSYETLYANGSRRTETQVGIYILSSSGDGAQHRDSGS 120

Db 61 VSSSCGPOCHKGTPLPTVEEAKQYLSYETLYANGSRRTETQVGIYILSSSGDGAQHRDSGS 120

QY 121 SGKSRKQIYGYDSRFSIFGKDFLLNYPFSTSVKLSCTGCTGLVAEKHVLTAACHIDHG 180

Db 121 SGKSRKQIYGYDSRFSIFGKDFLLNYPFSTSVKLSCTGCTGLVAEKHVLTAACHIDHG 180

QY 181 KTYVVGTKLRVGFLLKPKFKDGGRGANDSTAMPQMKFQWIRVKTHTVPKGIKGNAND 240

Db 181 KTYVVGTKLRVGFLLKPKFKDGGRGANDSTAMPQMKFQWIRVKTHTVPKGIKGNAND 240

QY 241 IGMWDYDIALLELKPKHKKFKMKIGVSPPAKQIPGGRIHPSGYDNDPQGNLVYRFGCDVKDE 300

Db 241 IGMWDYDIALLELKPKHKKFKMKIGVSPPAKQIPGGRIHPSGYDNDPQGNLVYRFGCDVKDE 300

QY 301 TYDLLYQQCDAQPGASGSGVYVVMKRRQQQKWERKLIIGIFSGHQWDMNGSPQDFNVAVR 360

Db 301 TYDLLYQQCDAQPGASGSGVYVVMKRRQQQKWERKLIIGIFSGHQWDMNGSPQDFNVAVR 360

QY 361 ITPLKYAQICYWIKGNLYDCREG 383

Db 361 ITPLKYAQICYWIKGNLYDCREG 383

RESULT 14

AAU29048

ID AAU29048 standard; protein; 383 AA.

XX AC AAU29048;

XX DT 18-DEC-2001 (first entry)

XX DE Human PRO polypeptide sequence #25.

XX PRO polypeptide; mammal; tumour; cancer; human; cattle; horse; sheep;

KW dog; cat; pig; goat; rabbit; tumour necrosis factor alpha; TNF-alpha;

KW blood; chondrocyte cell; cell proliferation; cell differentiation; colon;

KW adrenal; lung; breast; prostate; rectum; cervix; liver; genetic disorder.

XX OS Homo sapiens.

XX PN WO200168848-A2.

XX PD 20-SEP-2001.

XX PF 28-FEB-2001; 2001WO-US006520.

XX PR 01-MAR-2000; 2000WO-US005601.

PR 02-MAR-2000; 2000WO-US005841.

PR 03-MAR-2000; 2000US-0187202P.

PR 06-MAR-2000; 2000US-0186968P.

PR 14-MAR-2000; 2000US-0189120P.

PR 14-MAR-2000; 2000US-0189128P.

PR 15-MAR-2000; 2000WO-US006884.

PR 21-MAR-2000; 2000US-0190828P.

PR 21-MAR-2000; 2000US-0191007P.

PR 21-MAR-2000; 2000US-0191048P.

PR 21-MAR-2000; 2000US-0191314P.

PR 28-MAR-2000; 2000US-0192655P.

PR 29-MAR-2000; 2000US-0193032P.

PR 29-MAR-2000; 2000US-0193053P.

PR 30-MAR-2000; 2000WO-US008439.

PR 04-APR-2000; 2000US-0194449P.

PR 04-APR-2000; 2000US-0194647P.

PR 11-APR-2000; 2000US-0195975P.

PR 11-APR-2000; 2000US-0196000P.

PR 11-APR-2000; 2000US-0196187P.

PR 11-APR-2000; 2000US-0196690P.

PR 18-APR-2000; 2000US-0196820P.

PR 18-APR-2000; 2000US-0198121P.

PR 18-APR-2000; 2000US-0198585P.

PR 25-APR-2000; 2000US-0199397P.

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PR 25-APR-2000; 2000US-0199550P.
PR 25-APR-2000; 2000US-0199654P.
PR 03-MAY-2000; 2000US-0201516P.
PR 17-MAY-2000; 2000WO-US01370S.
PR 22-MAY-2000; 2000WO-US014042.
PR 30-MAY-2000; 2000WO-US014941.
PR 02-JUN-2000; 2000WO-US015264.
PR 05-JUN-2000; 2000US-0209832P.
PR 28-JUL-2000; 2000US-02020710.
PR 22-AUG-2000; 2000US-00644848.
PR 24-AUG-2000; 2000WO-US023328.
PR 08-NOV-2000; 2000WO-US030952.
PR 01-DEC-2000; 2000WO-US032678.
PR 20-DEC-2000; 2000WO-US034956.
XX (GETH ) GENENTECH INC.
XX
XX Baker KP, Chen J, Desnoyers L, Goddard A, Godowski PJ, Gurney AL;
PI Pan J, Smith V, Watanabe CK, Wood WI, Zhang Z;
XX
XX WPI; 2001-602746/68.
XX N-PSDB; AAS45949.
XX
XX Novel nucleic acids encoding PRO polypeptides, used to diagnose the
PT presence of tumors, such as prostate and breast tumors, in mammals and to
PT screen for modulators of the compounds.
XX
XX Claim 11; Fig 50; 774pp; English.
XX
XX Sequences AAU29024-AAU29328 represent PRO polypeptides of the invention.
CC The PRO polypeptides and their associated nucleic acids can be used to
CC detect the presence of a tumour in a mammal by comparing the level of
CC expression of a PRO polypeptide in a test sample of cells from the animal
CC and a control sample of normal cells, whereby a higher level of
CC expression in the test sample indicates the presence of a tumour in the
CC mammal. Mammals include dogs, cats, cattle, horses, sheep, pigs, goats
CC and rabbits but are preferably human. The polypeptides can be used to
CC stimulate tumour necrosis factor (TNF) alpha release from human blood,
CC when contacted with it. A specific polypeptide can be used to stimulate
CC the proliferation or differentiation of chondrocyte cells. The PRO
CC proteins can be used to determine the presence of tumours and also
CC susceptibility to tumour development, particularly adrenal, lung, colon,
CC breast, prostate, cervical or liver tumours, in mammalian
CC subjects. The oligonucleotide probes specific for the PRO nucleic acids
CC can be used for genetic analysis of individuals with genetic disorders
XX
XX Sequence 383 AA;
Query Match 97.6%; Score 2080; DB 4; Length 383;
Best Local Similarity 100.0%; Pred. No. 2.8e-147;
Matches 383; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 1 MAGIPGLLFLLLCAVGVQSPYSAPWKTWPAYRLPVVLPQSTLNLAKEPFGAEAKLE 60
QY 61 VSSSCGPQCHKGTPLPTYEAKYLSYETLIYANGSRTETQVGIYILSSSGDGAQHRDGS 120
DB 61 VSSSCGPQCHKGTPLPTYEAKYLSYETLIYANGSRTETQVGIYILSSSGDGAQHRDGS 120
QY 121 SGKSRKRIQYGVDSRFSFGKDFLLNYPSTSVKLTGCTGTLVAEKHVLTAACHIHG 180
DB 121 SGKSRKRIQYGVDSRFSFGKDFLLNYPSTSVKLTGCTGTLVAEKHVLTAACHIHG 180
QY 181 KTVVKGTKLVRGFLKPKFKDGRGANDSTSAPEQMKFOWIRVKVTHVPKGIKNAND 240
DB 181 KTVVKGTKLVRGFLKPKFKDGRGANDSTSAPEQMKFOWIRVKVTHVPKGIKNAND 240
QY 241 IGMVDYVALLLEKKPHKPKMKI GVSPPAKQLPGGR IHFSGYDNDPRGNLVYRFDVKDE 300
DB 241 IGMVDYVALLLEKKPHKPKMKI GVSPPAKQLPGGR IHFSGYDNDPRGNLVYRFDVKDE 300
QY 301 TYDLLYQQCDAQGASGSGVYVRWKRQOQKWERKIIGIFSGHQWDMNGSPQDFNVAVR 360
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DB 301 TYDLLYQQCDAQGASGSGVYVRWKRQOQKWERKIIGIFSGHQWDMNGSPQDFNVAVR 360
QY 361 ITPLKYAQICYWIKGNLYDCREG 383
DB 361 ITPLKYAQICYWIKGNLYDCREG 383
RESULT 15
ABUS8424
ID ABUS8424 standard; protein; 383 AA.
XX
XX AC ABUS8424;
XX
XX DT 15-APR-2003 (first entry)
XX
XX Human PRO polypeptide #25.
XX
XX Human; PRO; cytostatic; tumour; cancer; breast; lung; stomach; liver;
XX dog; cat; cow; horse; sheep; pig; goat; rabbit; ADERT;
XX antibody-dependent enzyme mediated prodruug therapy.
XX
XX Homo sapiens.
XX
XX US2003027272-A1.
XX
XX 06-FEB-2003.
XX
XX 21-JUN-2002; 2002US-00176492.
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XX 18-SEP-1997; 97US-0059263P.
XX 18-SEP-1997; 97US-0059266P.
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XX 24-NOV-1997; 97US-0066772P.
XX 11-DEC-1997; 97US-0069335P.
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XX 01-APR-1998; 98US-0080333P.
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Db	181	KTYVKGTKLRVGLPKPKFDGGGANDSTSAMPEQMKFQWIRVKRTHVPEKGIKGNAND	240
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Db	241	IGMDYDVALLELKKPHKRKFKMKIGVSPPAKQLPGGRIFHSGYDNDPRGNLVYRFCVXDE	300
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Qy	361	ITPLKYAQCICYWIKNYLDREG	383
Db	361	ITPLKYAQCICYWIKNYLDREG	383

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Job time : 102.435 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 1, 2005, 20:57:14 ; Search time 26.5364 Seconds
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1102.727 Million cell updates/sec

Title: US-09-658-677-15

Perfect score: 2131

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Scoring table: BLOSUM62

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Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2131	100.0	392	3	US-09-072-384-15
2	2085	97.8	392	3	Sequence 2, Appli
3	2080	97.6	383	3	Sequence 18, Appl
4	2080	97.6	383	4	US-09-072-384-18
5	2080	97.6	383	4	Sequence 261, App
6	2080	97.6	383	4	US-09-072-384-261
7	2080	97.6	383	4	Sequence 261, App
8	2080	97.6	383	4	US-09-072-384-261
9	2080	97.6	383	4	Sequence 261, App
10	2080	97.6	383	4	US-09-072-384-261
11	2080	97.6	383	4	Sequence 261, App
12	2080	97.6	383	4	US-09-072-384-261
13	202.5	9.5	314	4	US-09-072-384-261
14	193	9.1	316	4	US-09-072-384-261
15	177	8.3	222	1	US-08-090-048-1
16	177	8.3	222	2	US-08-292-550-1
17	177	8.3	222	2	US-07-927-661A-1
18	176.5	8.3	318	4	US-09-551-826D-10
19	140.5	6.6	239	4	US-09-107-433-3471
20	135.5	6.4	313	4	US-09-551-826D-14
21	132	6.2	218	4	US-09-551-826D-14
22	129.5	6.1	302	4	US-09-551-826D-12
23	129	6.1	433	4	US-09-551-826D-12
24	127	6.0	303	4	US-09-551-826D-8
25	127	6.0	320	4	US-09-489-039A-13989
26	126.5	5.9	356	4	US-09-002-540-12881
27	122.5	5.7	238	4	US-09-664-595A-15

28 122 5.7 256 3 US-08-906-769-89 Sequence 89, Appl
29 122 5.7 256 3 US-08-906-616-89 Sequence 89, Appl
30 122 5.7 256 3 US-08-817-795-89 Sequence 89, Appl
31 122 5.7 256 3 US-08-639-075A-89 Sequence 89, Appl
32 122 5.7 256 3 US-09-012-431-89 Sequence 32, Appl
33 122 5.7 256 3 US-09-032-215-32 Sequence 89, Appl
34 122 5.7 256 3 US-09-012-692-89 Sequence 89, Appl
35 122 5.7 256 3 US-08-906-613-89 Sequence 89, Appl
36 122 5.7 256 5 PCT-US95-1442A-89 Sequence 89, Appl
37 120 5.6 284 4 US-09-387-375-7 Sequence 7, Appl
38 120 5.6 284 4 US-10-041-400A-7 Sequence 7, Appl
39 120 5.6 284 4 US-10-042-091A-7 Sequence 7, Appl
40 117 5.5 437 1 US-08-487-037-2 Sequence 2, Appl
41 115.5 5.4 241 3 US-08-944-483-59 Sequence 59, Appl
42 114 5.3 228 3 US-08-944-483-44 Sequence 44, Appl
43 114 5.3 253 6 5223425-8 Patent No. 5223425
44 114 5.3 253 6 5223425-8 Patent No. 5223425
45 113 5.3 238 6 5223425-5 Patent No. 5223425

ALIGNMENTS

RESULT 1
US-09-072-384-15
; Sequence 15, Application US/09072384
; Patent No. 6153420
; GENERAL INFORMATION:
; APPLICANT: Sheppard, Paul O.
; TITLE OF INVENTION: SERINE PROTEASE POLYPEPTIDES
; TITLE OF INVENTION: AND MATERIALS AND METHODS FOR MAKING THEM
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ZymoGenetics, Inc.
; STREET: 1201 Eastlake Avenue East
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98102
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/072,384
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Parker, Gary E
; REGISTRATION NUMBER: 31,648
; REFERENCE/DOCKET NUMBER: 97-16CI
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-442-6673
; TELEFAX: 206-442-6678
; TELEX:
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 392 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
; FEATURE:
; NAME/KEY: Signal Sequence
; LOCATION: 1..19
; OTHER INFORMATION:
US-09-072-384-15

Query Match 100.0%; Score 2131; DB 3; Length 392;
Best Local Similarity 100.0%; Pred. No. 1.5e-225;
Matches 392; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAGIPGLFLFLFLLCAVGVSPYSAPWKPTWPAYRLPVVLPQSTLNLAQPDGAEAKLE 60
DB 1 MAGIPGLFLFLFLLCAVGVSPYSAPWKPTWPAYRLPVVLPQSTLNLAQPDGAEAKLE 60

QY 61 VSSSCGPQCHKGTPPTVEEAKQYLSYETLYANGSRTEQVGIYILSSSGDGAQHRS DGS 120
DB 61 VSSSCGPQCHKGTPPTVEEAKQYLSYETLYANGSRTEQVGIYILSSSGDGAQHRS DGS 120

QY 121 SGKSRKRQIYGYDSRFSIFGKDFLLNYPFSTSVKLSCTGTLVAEKHVLTAACHIDG 180
DB 121 SGKSRKRQIYGYDSRFSIFGKDFLLNYPFSTSVKLSCTGTLVAEKHVLTAACHIDG 180

QY 181 KTVYVGTOKLVRGFLKPKFKDGGGRANDSTSAMPEQMKFQWIRVKTHTVPKGIKNAND 240
DB 181 KTVYVGTOKLVRGFLKPKFKDGGGRANDSTSAMPEQMKFQWIRVKTHTVPKGIKNAND 240

QY 241 IGMDDYDYLLELKKPKFKMKGIVSPPAKQLPGGRIHFSGYDNDPRGNLVYRFCVDKDE 300
DB 241 IGMDDYDYLLELKKPKFKMKGIVSPPAKQLPGGRIHFSGYDNDPRGNLVYRFCVDKDE 300

QY 301 TYDLLYQCCDAQPGASGSGVYVWMKROQKWKRIIGIFSGHQWDMNGSPQDFNVAVR 360
DB 301 TYDLLYQCCDAQPGASGSGVYVWMKROQKWKRIIGIFSGHQWDMNGSPQDFNVAVR 360

QY 361 ITPKYAQICYWKGNLYDCREGDTVFPPGNS 392
DB 361 ITPKYAQICYWKGNLYDCREGDTVFPPGNS 392

RESULT 2

US-09-072-384-2
; Sequence 2, Application US/09072384
; Patent No. 6153420
; GENERAL INFORMATION:
; APPLICANT: Sheppard, Paul O.
; TITLE OF INVENTION: SERINE PROTEASE POLYPEPTIDES
; TITLE OF INVENTION: AND MATERIALS AND METHODS FOR MAKING THEM
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ZymoGenetics, Inc.
; STREET: 1201 Eastlake Avenue East
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98102
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/072,384
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Parker, Gary E
; REGISTRATION NUMBER: 31,648
; REFERENCE/DOCKET NUMBER: 97-16C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-442-6673
; TELEFAX: 206-442-6678
; TELEX:
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 392 amino acids
; TYPE: amino acid

STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
FRAGMENT TYPE: internal
FEATURE:
NAME/KEY: Signal Sequence
LOCATION: 1...19
OTHER INFORMATION:
US-09-072-384-2

Query Match 97.8%; Score 2085; DB 3; Length 392;
Best Local Similarity 98.2%; Pred. No. 1.8e-220;
Matches 385; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 1 MAGIPGLFLFLFLLCAVGVSPYSAPWKPTWPAYRLPVVLPQSTLNLAQPDGAEAKLE 60
DB 1 MAGIPGLFLFLFLLCAVGVSPYSAPWKPTWPAYRLPVVLPQSTLNLAQPDGAEAKLE 60

QY 61 VSSSCGPQCHKGTPPTVEEAKQYLSYETLYANGSRTEQVGIYILSSSGDGAQHRS DGS 120
DB 61 VSSSCGPQCHKGTPPTVEEAKQYLSYETLYANGSRTEQVGIYILSSSGDGAQHRS DGS 120

QY 121 SGKSRKRQIYGYDSRFSIFGKDFLLNYPFSTSVKLSCTGTLVAEKHVLTAACHIDG 180
DB 121 SGKSRKRQIYGYDSRFSIFGKDFLLNYPFSTSVKLSCTGTLVAEKHVLTAACHIDG 180

QY 181 KTVYVGTOKLVRGFLKPKFKDGGGRANDSTSAMPEQMKFQWIRVKTHTVPKGIKNAND 240
DB 181 KTVYVGTOKLVRGFLKPKFKDGGGRANDSTSAMPEQMKFQWIRVKTHTVPKGIKNAND 240

QY 241 IGMDDYDYLLELKKPKFKMKGIVSPPAKQLPGGRIHFSGYDNDPRGNLVYRFCVDKDE 300
DB 241 IGMDDYDYLLELKKPKFKMKGIVSPPAKQLPGGRIHFSGYDNDPRGNLVYRFCVDKDE 300

QY 301 TYDLLYQCCDAQPGASGSGVYVWMKROQKWKRIIGIFSGHQWDMNGSPQDFNVAVR 360
DB 301 TYDLLYQCCDAQPGASGSGVYVWMKROQKWKRIIGIFSGHQWDMNGSPQDFNVAVR 360

QY 361 ITPKYAQICYWKGNLYDCREGDTVFPPGNS 392
DB 361 ITPKYAQICYWKGNLYDCREGDTVFPPGNS 392

RESULT 3

US-09-072-384-18
; Sequence 18, Application US/09072384
; Patent No. 6153420
; GENERAL INFORMATION:
; APPLICANT: Sheppard, Paul O.
; TITLE OF INVENTION: SERINE PROTEASE POLYPEPTIDES
; TITLE OF INVENTION: AND MATERIALS AND METHODS FOR MAKING THEM
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ZymoGenetics, Inc.
; STREET: 1201 Eastlake Avenue East
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98102
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/072,384
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Parker, Gary E

REGISTRATION NUMBER: 31,648
 REFERENCE/DOCKET NUMBER: 97-16C1
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 206-442-6673
 TELEFAX: 206-442-6678
 TELEX:
 INFORMATION FOR SEQ ID NO: 18:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 383 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 FRAGMENT TYPE: internal
 FEATURE:
 NAME/KEY: Signal Sequence
 LOCATION: 1...19
 OTHER INFORMATION:
 US-09-072-384-18

Query Match 97.6%; Score 2080; DB 3; Length 383;
 Best Local Similarity 100.0%; Pred. No. 6e-220;
 Matches 383; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAGIPGLLFLFLLCAGGVSPYSAPWKPPTWPAYRLPVVLPSTLNLAKEPFGAEAKLE 60
 DB 1 MAGIPGLLFLFLLCAGGVSPYSAPWKPPTWPAYRLPVVLPSTLNLAKEPFGAEAKLE 60

QY 61 VSSSCGPGCHKGTPPTPYEAKQYLSYETLYANGSRSTETQVGIYILSSGSGAQHRDGS 120
 DB 61 VSSSCGPGCHKGTPPTPYEAKQYLSYETLYANGSRSTETQVGIYILSSGSGAQHRDGS 120

QY 121 SGKSRKRQIYGYDSRFSIFGKDFLLNYPSTSVKLSCTGTGLVAEKHVLTAACHIDG 180
 DB 121 SGKSRKRQIYGYDSRFSIFGKDFLLNYPSTSVKLSCTGTGLVAEKHVLTAACHIDG 180

QY 181 KTYVKGTKLRVGLFKPKFKDGGGRANDSTAMPQMKFQWIRKTRHVPKGIKGNAND 240
 DB 181 KTYVKGTKLRVGLFKPKFKDGGGRANDSTAMPQMKFQWIRKTRHVPKGIKGNAND 240

QY 241 IGMDDYALLELKKPKHKFMKIGVSPPAKQLPGGRIFHSGYDNDPRGNLVYRFDVKDE 300
 DB 241 IGMDDYALLELKKPKHKFMKIGVSPPAKQLPGGRIFHSGYDNDPRGNLVYRFDVKDE 300

QY 301 TYDLLYQCDAPGASGSGVYVWRWKQKQKWKIIFSGHQMVGDMGSPQDFNVAVR 360
 DB 301 TYDLLYQCDAPGASGSGVYVWRWKQKQKWKIIFSGHQMVGDMGSPQDFNVAVR 360

QY 361 ITPLKVAQICWIKGNVLDREG 383
 DB 361 ITPLKVAQICWIKGNVLDREG 383

RESULT 4
 US-09-907-794A-261
 Sequence 261, Application US/09907794A
 Patent No. 6635468
 GENERAL INFORMATION:
 APPLICANT: Genentech, Inc.
 APPLICANT: Ashkenazi, Avi
 APPLICANT: Botstein, David
 APPLICANT: Desnoyers, Luc
 APPLICANT: Eaton, Dan L.
 APPLICANT: Ferrara, Napoleone
 APPLICANT: Filvaroff, Ellen
 APPLICANT: Fong, Sherman
 APPLICANT: Gao, Wei-Qiang
 APPLICANT: Gerber, Hanpeter
 APPLICANT: Gerritsen, Mary E.
 APPLICANT: Goddard, A.
 APPLICANT: Godowaki, Paul J.
 APPLICANT: Grimaldi, Christopher J.
 APPLICANT: Gurney, Austin L.

APPLICANT: Hillan, Kenneth, J.
 APPLICANT: Kljavin, Ivar J.
 APPLICANT: Mather, Jemie P.
 APPLICANT: Pan, James
 APPLICANT: Paoni, Nicholas F.
 APPLICANT: Roy, Margaret Ann
 APPLICANT: Stewart, Timothy A.
 APPLICANT: Tumas, Daniel
 APPLICANT: Williams, P. Mickey
 APPLICANT: Wood, William, I.
 TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
 FILE OF INVENTION: Acids Encoding the Same
 FILE REFERENCE: 10466-14
 CURRENT APPLICATION NUMBER: US/09/907,794A
 CURRENT FILING DATE: 2001-07-17
 PRIOR APPLICATION NUMBER: PCT/US00/04414
 PRIOR FILING DATE: 2000-02-22
 PRIOR APPLICATION NUMBER: US 60/143,048
 PRIOR FILING DATE: 1999-07-07
 PRIOR APPLICATION NUMBER: US 60/145,698
 PRIOR FILING DATE: 1999-07-26
 PRIOR APPLICATION NUMBER: US 60/146,222
 PRIOR FILING DATE: 1999-07-28
 PRIOR APPLICATION NUMBER: PCT/US99/20594
 PRIOR FILING DATE: 1999-09-08
 PRIOR APPLICATION NUMBER: PCT/US99/20944
 PRIOR FILING DATE: 1999-09-13
 PRIOR APPLICATION NUMBER: PCT/US99/21090
 PRIOR FILING DATE: 1999-09-15
 PRIOR APPLICATION NUMBER: PCT/US99/21547
 PRIOR FILING DATE: 1999-09-15
 PRIOR APPLICATION NUMBER: PCT/US99/23089
 PRIOR FILING DATE: 1999-10-05
 PRIOR APPLICATION NUMBER: PCT/US99/28214
 PRIOR FILING DATE: 1999-11-29
 PRIOR APPLICATION NUMBER: PCT/US99/28313
 PRIOR FILING DATE: 1999-11-30
 PRIOR APPLICATION NUMBER: PCT/US99/28564
 PRIOR FILING DATE: 1999-12-02
 PRIOR APPLICATION NUMBER: PCT/US99/28565
 PRIOR FILING DATE: 1999-12-02
 PRIOR APPLICATION NUMBER: PCT/US99/30095
 PRIOR FILING DATE: 1999-12-16
 PRIOR APPLICATION NUMBER: PCT/US99/30911
 PRIOR FILING DATE: 1999-12-20
 PRIOR APPLICATION NUMBER: PCT/US99/30999
 PRIOR FILING DATE: 1999-12-20
 PRIOR APPLICATION NUMBER: PCT/US00/00219
 PRIOR FILING DATE: 2000-01-05
 NUMBER OF SEQ ID NOS: 423
 SEQ ID NO 261
 LENGTH: 383
 TYPE: PRT
 ORGANISM: Homo Sapien
 US-09-907-794A-261

Query Match 97.6%; Score 2080; DB 4; Length 383;
 Best Local Similarity 100.0%; Pred. No. 6e-220;
 Matches 383; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAGIPGLLFLFLLCAGGVSPYSAPWKPPTWPAYRLPVVLPSTLNLAKEPFGAEAKLE 60
 DB 1 MAGIPGLLFLFLLCAGGVSPYSAPWKPPTWPAYRLPVVLPSTLNLAKEPFGAEAKLE 60

QY 61 VSSSCGPGCHKGTPPTPYEAKQYLSYETLYANGSRSTETQVGIYILSSGSGAQHRDGS 120
 DB 61 VSSSCGPGCHKGTPPTPYEAKQYLSYETLYANGSRSTETQVGIYILSSGSGAQHRDGS 120

QY 121 SGKSRKRQIYGYDSRFSIFGKDFLLNYPSTSVKLSCTGTGLVAEKHVLTAACHIDG 180
 DB 121 SGKSRKRQIYGYDSRFSIFGKDFLLNYPSTSVKLSCTGTGLVAEKHVLTAACHIDG 180

QY 181 KTYVKGTKLRVGLFKPKFKDGGGRANDSTAMPQMKFQWIRKTRHVPKGIKGNAND 240

Db 181 KTVYVGTQKLVGFLKPKFQDGGGRANDSTSAPEQMKFQWIRVKTHTVPGWIKGNAND 240
QY 241 IGMDDYALLELKKPKRKFPMKIGVSPPAKQLPGRIRHFSGYDNDPRPGLNLYVRFCDVKDE 300
Db 241 IGMDDYALLELKKPKRKFPMKIGVSPPAKQLPGRIRHFSGYDNDPRPGLNLYVRFCDVKDE 300
QY 301 TYDLLYQQCDAQPGAGSGGVYVVMWKRQQQKWERKIIGIFSGHQWDMNGSPQDFNVAVR 360
Db 301 TYDLLYQQCDAQPGAGSGGVYVVMWKRQQQKWERKIIGIFSGHQWDMNGSPQDFNVAVR 360
QY 361 ITPLKYAQICYWIKGNLYDCREG 383
Db 361 ITPLKYAQICYWIKGNLYDCREG 383

RESULT 5
US-09-905-125A-261
; Sequence 261, Application US/09905125A
; Patent No. 6664376
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Baton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/905,125A
; PRIOR FILING DATE: 2001-07-12
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30

; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 261
; LENGTH: 383
; TYPE: PRT
; ORGANISM: Homo Sapien
US-09-905-125A-261
Query Match 97.6%; Score 2080; DB 4; Length 383;
Best Local Similarity 100.0%; Pred. No. 6e-220;
Matches 383; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MAGIFGLLELLFLLCAVGVSPYAPWKPTWPAYRLPVVLPQSTLNLAKPDPGAEAKLE 60
Db 1 MAGIFGLLELLFLLCAVGVSPYAPWKPTWPAYRLPVVLPQSTLNLAKPDPGAEAKLE 60
QY 61 VSSSGCPQCHKGTPLTPTTBEAAQYLSYETLYANGSRTEQVGIYILSSSGDGAQHRDSSG 120
Db 61 VSSSGCPQCHKGTPLTPTTBEAAQYLSYETLYANGSRTEQVGIYILSSSGDGAQHRDSSG 120
QY 121 SGKSRKRQIYGYDSRFSIFGKDFLLNYPFSTSVKLSTGCTGTLVAEKHVLTAACHIDG 180
Db 121 SGKSRKRQIYGYDSRFSIFGKDFLLNYPFSTSVKLSTGCTGTLVAEKHVLTAACHIDG 180
QY 181 KTYVGTQKLVGFLKPKFQDGGGRANDSTSAPEQMKFQWIRVKTHTVPGWIKGNAND 240
Db 181 KTYVGTQKLVGFLKPKFQDGGGRANDSTSAPEQMKFQWIRVKTHTVPGWIKGNAND 240
QY 241 IGMDDYALLELKKPKRKFPMKIGVSPPAKQLPGRIRHFSGYDNDPRPGLNLYVRFCDVKDE 300
Db 241 IGMDDYALLELKKPKRKFPMKIGVSPPAKQLPGRIRHFSGYDNDPRPGLNLYVRFCDVKDE 300
QY 301 TYDLLYQQCDAQPGAGSGGVYVVMWKRQQQKWERKIIGIFSGHQWDMNGSPQDFNVAVR 360
Db 301 TYDLLYQQCDAQPGAGSGGVYVVMWKRQQQKWERKIIGIFSGHQWDMNGSPQDFNVAVR 360
QY 361 ITPLKYAQICYWIKGNLYDCREG 383
Db 361 ITPLKYAQICYWIKGNLYDCREG 383

RESULT 6
US-09-902-775A-261
; Sequence 261, Application US/09902775A
; Patent No. 6686451
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Baton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.

```
APPLICANT: Kljavin, Ivar J.
APPLICANT: Mather, Jennie P.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: 10466-14
CURRENT APPLICATION NUMBER: US/09/902,775A
PRIOR FILING DATE: 2001-07-10
PRIOR APPLICATION NUMBER: PCT/US00/04414
PRIOR FILING DATE: 2000-02-22
PRIOR APPLICATION NUMBER: US 60/143,048
PRIOR FILING DATE: 1999-07-07
PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR FILING DATE: 1999-07-26
PRIOR APPLICATION NUMBER: US 60/146,222
PRIOR FILING DATE: 1999-07-28
PRIOR APPLICATION NUMBER: PCT/US99/20594
PRIOR FILING DATE: 1999-09-08
PRIOR APPLICATION NUMBER: PCT/US99/20944
PRIOR FILING DATE: 1999-09-13
PRIOR APPLICATION NUMBER: PCT/US99/21090
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/21547
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/23089
PRIOR FILING DATE: 1999-10-05
PRIOR APPLICATION NUMBER: PCT/US99/28214
PRIOR FILING DATE: 1999-11-29
PRIOR APPLICATION NUMBER: PCT/US99/28313
PRIOR FILING DATE: 1999-11-30
PRIOR APPLICATION NUMBER: PCT/US99/28564
PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/28565
PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/30095
PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: PCT/US99/30911
PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US99/30999
PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US00/00219
PRIOR FILING DATE: 2000-01-05
NUMBER OF SEQ ID NOS: 423
SEQ ID NO 261
LENGTH: 383
TYPE: PRT
ORGANISM: Homo Sapien
US-09-902-775A-261

Query Match          97.6%; Score 2080; DB 4; Length 383;
Best Local Similarity 100.0%; Pred. No. 6e-220;
Matches 383; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1  MAGIPGLLFLFLLCAGGVSPYAPWKPWPAYRLPVVLPSTLNLAQDFGAEAQLE 60
DB      1  MAGIPGLLFLFLLCAGGVSPYAPWKPWPAYRLPVVLPSTLNLAQDFGAEAQLE 60

QY      61  VSSSCGPGQCHKGTPLPTYEAKQYLSYETLYANGSRRTQVGIIYILSSSGDGAQHRDGS 120
DB      61  VSSSCGPGQCHKGTPLPTYEAKQYLSYETLYANGSRRTQVGIIYILSSSGDGAQHRDGS 120

QY      121  SGKSRKRQIYGVDSRFSIFGKDFLLNYPSTSVKLSGTGCTGLVAEKHVLTAACHIDG 180
DB      121  SGKSRKRQIYGVDSRFSIFGKDFLLNYPSTSVKLSGTGCTGLVAEKHVLTAACHIDG 180

QY      181  KTVVKGTKLVRGFLKPKFKDGGGRANDSTSAMPEQMKFQWIRVKRTHVPKGIKGNAND 240
DB      181  KTVVKGTKLVRGFLKPKFKDGGGRANDSTSAMPEQMKFQWIRVKRTHVPKGIKGNAND 240
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DB      181  KTVVKGTKLVRGFLKPKFKDGGGRANDSTSAMPEQMKFQWIRVKRTHVPKGIKGNAND 240
QY      241  IGMVDYDYLLELKKHKKFKMKIGVSPPAKQIPGGRIHESGYDNDPRPGLNLYVRFCDVKDE 300
DB      241  IGMVDYDYLLELKKHKKFKMKIGVSPPAKQIPGGRIHESGYDNDPRPGLNLYVRFCDVKDE 300
QY      301  TYDLLYQOCDAQAGSAGSGVYVMMKRCQOKWKRIIGIFSGHGWYDMNGSPQDFNVAVR 360
DB      301  TYDLLYQOCDAQAGSAGSGVYVMMKRCQOKWKRIIGIFSGHGWYDMNGSPQDFNVAVR 360
QY      361  ITPLKYAQICYWIKGNLYDCREG 383
DB      361  ITPLKYAQICYWIKGNLYDCREG 383

RESULT 7
US-09-906-700-261
; Sequence 261, Application US/09906700
; Patent No. 6723535
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/906,700
; PRIOR FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
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; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 261
; LENGTH: 383
; TYPE: PRT
; ORGANISM: Homo Sapien
US-09-906-700-261

Query Match
Best Local Similarity 97.6%; Score 2080; DB 4; Length 383;
Matches 383; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MAGIPGLLFLFLLCAVGVSPYSAPWKPPTWPAYRLPVVLPQSTLNLAQPDGAEAKLE 60
Db 1 MAGIPGLLFLFLLCAVGVSPYSAPWKPPTWPAYRLPVVLPQSTLNLAQPDGAEAKLE 60

Qy 61 VSSSCGPOCHKGTPLPTYEAAKQYLSYETLYANGSRTEQVGIYILSSSGDGAQHRDGS 120
Db 61 VSSSCGPOCHKGTPLPTYEAAKQYLSYETLYANGSRTEQVGIYILSSSGDGAQHRDGS 120

Qy 121 SGKSRKRQIYGYDSRFSIFGKDFLLNYPFSTSVKLSGTCTGLVAEKHVLTAACHIDG 180
Db 121 SGKSRKRQIYGYDSRFSIFGKDFLLNYPFSTSVKLSGTCTGLVAEKHVLTAACHIDG 180

Qy 181 KTYVKGTKLRVGFLLKPKFKDGGGRANDSTSAMPQMKFQWIRVKRTHVPKGIKNAND 240
Db 181 KTYVKGTKLRVGFLLKPKFKDGGGRANDSTSAMPQMKFQWIRVKRTHVPKGIKNAND 240

Qy 241 IGMDDYALLELKKPKHKKFMKIGVSPPAKQLPGGRIFHSFGYDNDPRGNLVYRFCVDKDE 300
Db 241 IGMDDYALLELKKPKHKKFMKIGVSPPAKQLPGGRIFHSFGYDNDPRGNLVYRFCVDKDE 300

Qy 301 TYDLLVQCCDAQPGASGSGYVYRWKRRQKQKWKRIIGIFSGHQWDMNGSPQDFNVAVR 360
Db 301 TYDLLVQCCDAQPGASGSGYVYRWKRRQKQKWKRIIGIFSGHQWDMNGSPQDFNVAVR 360

Qy 361 ITPKYAQICYWKIGNYLDREG 383
Db 361 ITPKYAQICYWKIGNYLDREG 383

RESULT 8
US-09-903-603A-261
; Sequence 261, Application US/09903603A
; Patent No. 6767995
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Aabkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.

; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: GNE.1618P2C12
; CURRENT APPLICATION NUMBER: US/09/903,603A
; CURRENT FILING DATE: 2001-07-11
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 261
; LENGTH: 383
; TYPE: PRT
; ORGANISM: Homo Sapien
US-09-903-603A-261

Query Match
Best Local Similarity 97.6%; Score 2080; DB 4; Length 383;
Matches 383; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MAGIPGLLFLFLLCAVGVSPYSAPWKPPTWPAYRLPVVLPQSTLNLAQPDGAEAKLE 60
Db 1 MAGIPGLLFLFLLCAVGVSPYSAPWKPPTWPAYRLPVVLPQSTLNLAQPDGAEAKLE 60

Qy 61 VSSSCGPOCHKGTPLPTYEAAKQYLSYETLYANGSRTEQVGIYILSSSGDGAQHRDGS 120
Db 61 VSSSCGPOCHKGTPLPTYEAAKQYLSYETLYANGSRTEQVGIYILSSSGDGAQHRDGS 120

Qy 121 SGKSRKRQIYGYDSRFSIFGKDFLLNYPFSTSVKLSGTCTGLVAEKHVLTAACHIDG 180
Db 121 SGKSRKRQIYGYDSRFSIFGKDFLLNYPFSTSVKLSGTCTGLVAEKHVLTAACHIDG 180

Qy 181 KTYVKGTKLRVGFLLKPKFKDGGGRANDSTSAMPQMKFQWIRVKRTHVPKGIKNAND 240
Db 181 KTYVKGTKLRVGFLLKPKFKDGGGRANDSTSAMPQMKFQWIRVKRTHVPKGIKNAND 240

QY 241 IGMDDYDVALLELKKPHKRFKMGVSPAKQLPGRIHFGSYDNDPRGNLVYRFDVKDE 300
Db 241 IGMDDYDVALLELKKPHKRFKMGVSPAKQLPGRIHFGSYDNDPRGNLVYRFDVKDE 300
QY 301 TYDLLYQQCDAQPGASGGVYVVMWKRQQQKWERKIIGIFSGHQMVDMMGSPQDFNVAVR 360
Db 301 TYDLLYQQCDAQPGASGGVYVVMWKRQQQKWERKIIGIFSGHQMVDMMGSPQDFNVAVR 360
QY 361 ITPLKYAQICYWIKGNLYDCREG 383
Db 361 ITPLKYAQICYWIKGNLYDCREG 383

RESULT 9

US-09-904-920A-261
; Sequence 261, Application US/09904920A
; Patent No. 6806352
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/904, 920A
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02

; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 261
; LENGTH: 383
; TYPE: PRT
; ORGANISM: Homo Sapien
US-09-904-920A-261
Query Match 97.6%; Score 2080; DB 4; Length 383;
Best Local Similarity 100.0%; Pred. No. 6e-220;
Matches 383; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MAGIPGLLFLFLLCAVGVSPYSAPWKPWPAYRLPVVLPSTLNLAKEPFGAEAKLE 60
Db 1 MAGIPGLLFLFLLCAVGVSPYSAPWKPWPAYRLPVVLPSTLNLAKEPFGAEAKLE 60
QY 61 VSSSCGPOCHKGTPLTYEAKQYLSYETLYANGSRTETQVGIYIILSSGCGAQRDGS 120
Db 61 VSSSCGPOCHKGTPLTYEAKQYLSYETLYANGSRTETQVGIYIILSSGCGAQRDGS 120
QY 121 SGKSRKROIYGYDSRFSIFGKDFLLNYPFSTSVKLSCTGTGLVAEKHVLTAACHIDG 180
Db 121 SGKSRKROIYGYDSRFSIFGKDFLLNYPFSTSVKLSCTGTGLVAEKHVLTAACHIDG 180
QY 181 KTYVKGTKLRVGFLLKPKFKDGGRGANDSTSAPEQMKFQWIRVKRTHVPKGIKGNAND 240
Db 181 KTYVKGTKLRVGFLLKPKFKDGGRGANDSTSAPEQMKFQWIRVKRTHVPKGIKGNAND 240
QY 241 IGMDDYDVALLELKKPHKRFKMGVSPAKQLPGRIHFGSYDNDPRGNLVYRFDVKDE 300
Db 241 IGMDDYDVALLELKKPHKRFKMGVSPAKQLPGRIHFGSYDNDPRGNLVYRFDVKDE 300
QY 301 TYDLLYQQCDAQPGASGGVYVVMWKRQQQKWERKIIGIFSGHQMVDMMGSPQDFNVAVR 360
Db 301 TYDLLYQQCDAQPGASGGVYVVMWKRQQQKWERKIIGIFSGHQMVDMMGSPQDFNVAVR 360
QY 361 ITPLKYAQICYWIKGNLYDCREG 383
Db 361 ITPLKYAQICYWIKGNLYDCREG 383

RESULT 10

US-09-909-064-261
; Sequence 261, Application US/09909064
; Patent No. 6818449
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.

APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: 10466-14
CURRENT APPLICATION NUMBER: US/09/909,064
PRIOR FILING DATE: 2001-07-18
PRIOR APPLICATION NUMBER: PCT/US00/04414
PRIOR FILING DATE: 2000-02-22
PRIOR APPLICATION NUMBER: US 60/143,048
PRIOR FILING DATE: 1999-07-07
PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR FILING DATE: 1999-07-26
PRIOR APPLICATION NUMBER: US 60/146,222
PRIOR FILING DATE: 1999-07-28
PRIOR APPLICATION NUMBER: PCT/US99/20594
PRIOR FILING DATE: 1999-09-08
PRIOR APPLICATION NUMBER: PCT/US99/20944
PRIOR FILING DATE: 1999-09-13
PRIOR APPLICATION NUMBER: PCT/US99/21090
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/21547
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/23089
PRIOR FILING DATE: 1999-10-05
PRIOR APPLICATION NUMBER: PCT/US99/28214
PRIOR FILING DATE: 1999-11-29
PRIOR APPLICATION NUMBER: PCT/US99/28313
PRIOR FILING DATE: 1999-11-30
PRIOR APPLICATION NUMBER: PCT/US99/28564
PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/28565
PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/30095
PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: PCT/US99/30911
PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US99/30999
PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US00/00219
PRIOR FILING DATE: 2000-01-05
NUMBER OF SEQ ID NOS: 423
SEQ ID NO 261
LENGTH: 383
TYPE: PRT
ORGANISM: Homo Sapien
US-09-909-064-261

Query Match 97.6% Score 2080; DB 4; Length 383;
Best Local Similarity 100.0%; Pred. No. 6e-220;
Matches 383; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAGIPGLLFLFLLCVAGQVSPSPAPKPTWPAAYRLPVVLPOSTLNLAQPDFAEAKLE 60
DB 1 MAGIPGLLFLFLLCVAGQVSPSPAPKPTWPAAYRLPVVLPOSTLNLAQPDFAEAKLE 60

QY 61 VSSSCGPGQCHKGTPLPYEEAKQYLSYETLYANGSRRTQVGYIILSSSGDGAQHRDGS 120
DB 61 VSSSCGPGQCHKGTPLPYEEAKQYLSYETLYANGSRRTQVGYIILSSSGDGAQHRDGS 120

QY 121 SGKSRKQIYGVDSRFSIFGKDFLNYPESTSVKLSCTGCTGLVAEKVLTAAHCIDHG 180
DB 121 SGKSRKQIYGVDSRFSIFGKDFLNYPESTSVKLSCTGCTGLVAEKVLTAAHCIDHG 180

QY 181 KTVVKGTKLRVGLFKPKFKDGGGRGANDSTSAMPEQMKFQWIRVKRTHVPKGIKGNAND 240
DB 181 KTVVKGTKLRVGLFKPKFKDGGGRGANDSTSAMPEQMKFQWIRVKRTHVPKGIKGNAND 240

QY 241 IGMVDYDVALLELKPKHKKFMKIGVSPRAKQLPGGRIHESGYDNDPRGNLVVRFCDVKDE 300
DB 241 IGMVDYDVALLELKPKHKKFMKIGVSPRAKQLPGGRIHESGYDNDPRGNLVVRFCDVKDE 300

QY 301 TYDLLYQQCDAQPGASGSGVYVVMWKRQOQKWERKIIGIFSGHQMVMNGSPQDFNVAVR 360
DB 301 TYDLLYQQCDAQPGASGSGVYVVMWKRQOQKWERKIIGIFSGHQMVMNGSPQDFNVAVR 360

QY 361 ITPLKYAQICYWIKGNLYLDCREG 383
DB 361 ITPLKYAQICYWIKGNLYLDCREG 383

RESULT 11
US-09-905-381A-261
Sequence 261, Application US/09905381A
Patent No. 6818746
GENERAL INFORMATION:
APPLICANT: Genentech, Inc.
APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, A.
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, Christopher J.
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth, J.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Mather, Jennie P.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: 10466-14
CURRENT APPLICATION NUMBER: US/09/905,381A
PRIOR FILING DATE: 2001-07-13
PRIOR APPLICATION NUMBER: PCT/US00/04414
PRIOR FILING DATE: 2000-02-22
PRIOR APPLICATION NUMBER: US 60/143,048
PRIOR FILING DATE: 1999-07-07
PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR FILING DATE: 1999-07-26
PRIOR APPLICATION NUMBER: US 60/146,222
PRIOR FILING DATE: 1999-07-28
PRIOR APPLICATION NUMBER: PCT/US99/20594
PRIOR FILING DATE: 1999-09-08
PRIOR APPLICATION NUMBER: PCT/US99/20944
PRIOR FILING DATE: 1999-09-13
PRIOR APPLICATION NUMBER: PCT/US99/21090
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/21547
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/23089
PRIOR FILING DATE: 1999-10-05
PRIOR APPLICATION NUMBER: PCT/US99/28214
PRIOR FILING DATE: 1999-11-29
PRIOR APPLICATION NUMBER: PCT/US99/28313
PRIOR FILING DATE: 1999-11-30
PRIOR APPLICATION NUMBER: PCT/US99/28564
PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/28565

; PRIOR FILING DATE: 1999-12-02
; -PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 261
; LENGTH: 383
; TYPE: PRT
; ORGANISM: Homo Sapien
US-09-905-381A-261

Query Match 97.6%; Score 2080; DB 4; Length 383;
Best Local Similarity 100.0%; Pred. No. 6e-220;
Matches 383; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 61 VSSSCGPOCHKGTPLTYEEAKQVLSYETLYANGSRTEQVGIYILSSSGDGAQHRDGS 120
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QY 121 SGKSRKRQIYGVDSRFSIFGKDFLLNYPFSTSVKLTGCTGTVAEKHVLTAACHIDG 180
DB 121 SGKSRKRQIYGVDSRFSIFGKDFLLNYPFSTSVKLTGCTGTVAEKHVLTAACHIDG 180
QY 181 KTYVKGTKLVGFLKPKFKDGGRGANDSTSAMPEQMKFQWIRVKTHTVPGKIKGNAND 240
DB 181 KTYVKGTKLVGFLKPKFKDGGRGANDSTSAMPEQMKFQWIRVKTHTVPGKIKGNAND 240
QY 241 IGMDDYDVALLELKKPHKRMKIGVSPPAKQLPGRIHFSGYDNDPGLNLYRFDCKDE 300
DB 241 IGMDDYDVALLELKKPHKRMKIGVSPPAKQLPGRIHFSGYDNDPGLNLYRFDCKDE 300
QY 301 TYDLYQQCDAQPCAGSGGVYVWMKRRQKQKWKRIIGIFSGHQWDMNGSPQDFNVAVR 360
DB 301 TYDLYQQCDAQPCAGSGGVYVWMKRRQKQKWKRIIGIFSGHQWDMNGSPQDFNVAVR 360
QY 361 ITPKVAQICWIKGNVLDREG 383
DB 361 ITPKVAQICWIKGNVLDREG 383

RESULT 12

US-09-906-618-261

; Sequence 261, Application US/09906618

; Patent No. 6828146

; GENERAL INFORMATION:

; APPLICANT: Genentech, Inc.

; APPLICANT: Ashkenazi, Avi

; APPLICANT: Botstein, David

; APPLICANT: Deans, Luc

; APPLICANT: Eaton, Dan L.

; APPLICANT: Ferrara, Napoleone

; APPLICANT: Filvaroff, Ellen

; APPLICANT: Fong, Sherman

; APPLICANT: Gao, Wei-Qiang

; APPLICANT: Gerber, Hanspeter

; APPLICANT: Gerritsen, Mary E.

; APPLICANT: Goddard, A.

; APPLICANT: Godowski, Paul J.

; APPLICANT: Grimaldi, Christopher J.

; APPLICANT: Gurney, Austin L.

; APPLICANT: Hillan, Kenneth, J.

; APPLICANT: Kljavin, Ivar J.

; APPLICANT: Mather, Jennie P.

; APPLICANT: Pan, James

; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/906,618
; CURRENT FILING DATE: 2001-07-16
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 261
; LENGTH: 383
; TYPE: PRT
; ORGANISM: Homo Sapien
US-09-906-618-261

Query Match 97.6%; Score 2080; DB 4; Length 383;
Best Local Similarity 100.0%; Pred. No. 6e-220;
Matches 383; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 MAGIPGLLEFLFLCAVGVSPYSAPWKPTWPAYRLPVVLPQSTLNLAKEPFGAEAKLE 60
QY 61 VSSSCGPOCHKGTPLTYEEAKQVLSYETLYANGSRTEQVGIYILSSSGDGAQHRDGS 120
DB 61 VSSSCGPOCHKGTPLTYEEAKQVLSYETLYANGSRTEQVGIYILSSSGDGAQHRDGS 120
QY 121 SGKSRKRQIYGVDSRFSIFGKDFLLNYPFSTSVKLTGCTGTVAEKHVLTAACHIDG 180
DB 121 SGKSRKRQIYGVDSRFSIFGKDFLLNYPFSTSVKLTGCTGTVAEKHVLTAACHIDG 180
QY 181 KTYVKGTKLVGFLKPKFKDGGRGANDSTSAMPEQMKFQWIRVKTHTVPGKIKGNAND 240
DB 181 KTYVKGTKLVGFLKPKFKDGGRGANDSTSAMPEQMKFQWIRVKTHTVPGKIKGNAND 240
QY 241 IGMDDYDVALLELKKPHKRMKIGVSPPAKQLPGRIHFSGYDNDPGLNLYRFDCKDE 300

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Db 241 IGMDDYDVALLELKKPHKRRKFMKIGVSPPAKQLPGRIHFGYDNDPRGNLVRFCVDVKE 300
Qy 301 TYDLLYQCCDAOPGASGGVYVVMWKRQOQKWERKIIGIFSGHQWYDMNGSPQDFNVAVR 360
Db 301 TYDLLYQCCDAOPGASGGVYVVMWKRQOQKWERKIIGIFSGHQWYDMNGSPQDFNVAVR 360
Qy 361 ITPKVAQICYWTKGNVLDREG 383
Db 361 ITPKVAQICYWTKGNVLDREG 383

RESULT 13
US-09-551-826D-6
; Sequence 6, Application US/09551826D.
; Patent No. 6558939
; GENERAL INFORMATION:
; APPLICANT: No. 6558939regaard-Madsen, Mads
; APPLICANT: Ostergaard, Peter Rahbek
; APPLICANT: Christensen, Claus Bo Voge
; APPLICANT: Lassen, Soren Flensated
; TITLE OF INVENTION: No. 6558939el Proteases And Variants Thereof
; FILE REFERENCE: 5665.200-US
; CURRENT APPLICATION NUMBER: US/09/551,826D
; CURRENT FILING DATE: 2000-04-17
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 6
; LENGTH: 314
; TYPE: PRT
; ORGANISM: Bacillus licheniformis AC116
US-09-551-826D-6

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Matches 77; Conservative 37; Mismatches 137; Indels 59; Gaps 13;

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Qy 133 YDSRFSIFGKDFLLNPFSTSVKLSLST---GCTTIVAEKHVLTAAACIHD-KTYTVKGTQ 188
Db 97 SDBERTVTD---TTAPFYRAIVHISISSIGCTGWLIGPKTVATAGHCYVDTSRSPAGTA 153

Qy 189 KLRVGLPKPKFKDGGRGANDSTSAMPEQMKFQIRVVRKTHVPKGMKGNANDIGMDYDVA 248
Db 154 TVSPG-----RNG-----SAYP-----YGSVTSTRYFIPSGWQSGNSN-----YDVA 190

Qy 249 LLELKKPHKRRKFMKIGVSPPAKQLPGRIHFGYDNDPRGNLVRFCD--VKDETYYDLLY 306
Db 191 AIELSQPIGNTVGYFGYSYVASSLAGAGVTISYCPGDKTTGTQWQMSGTIAVSETYKLOY 250

Qy 307 QCCDAOPGASGGVYVVMWKRQOQKWERKII-----GIFSGHQWYDMNGSPQDFNVAVRIT 362
Db 251 -AIDTYGGOSGSPVYKSSSRRTNCSGPCSLAVHTNGVYGG-----SSYNGRTRIT 299

Qy 363 PLKYAQCICW 372
Db 300 KEVDFNFTSW 309

RESULT 14
US-09-551-826D-2
; Sequence 2, Application US/09551826D
; Patent No. 6558939
; GENERAL INFORMATION:
; APPLICANT: No. 6558939regaard-Madsen, Mads
; APPLICANT: Ostergaard, Peter Rahbek
; APPLICANT: Christensen, Claus Bo Voge
; APPLICANT: Lassen, Soren Flensated
; TITLE OF INVENTION: No. 6558939el Proteases And Variants Thereof
; FILE REFERENCE: 5665.200-US
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; CURRENT APPLICATION NUMBER: US/09/551,826D
; CURRENT FILING DATE: 2000-04-17
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2
; LENGTH: 316
; TYPE: PRT
; ORGANISM: Bacillus licheniformis
US-09-551-826D-2

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Matches 79; Conservative 43; Mismatches 143; Indels 64; Gaps 15;

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Qy 120 SSGKRRKRQIYGYDSRFSIFGKDFLLN-----YPFSTSVKLSLST---GCTGTLVAKHV 170
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Qy 171 LTAACIHDGKT-YVKGTKLRVGLPKFKDGGRGANDSTSAMPEQMKFQIRVVRKTHV 229
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RESULT 15
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; Sequence 1, Application US/080900048
; Patent No. 5523237
; GENERAL INFORMATION:
; APPLICANT: Budtz, Peter
; APPLICANT: Nielsen, Per M.
; TITLE OF INVENTION: PROTEIN PREPARATIONS
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 5523237o No. 5523237disk of No. 5523237th America, Inc.
; STREET: 405 Lexington Avenue, 62nd Floor
; CITY: New York
; STATE: New York
; COUNTRY: United States of America
; ZIP: 10174-6201
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/090,048
; FILING DATE: 16-JUL-1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DK 199/91
; FILING DATE: 06-FEB-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/DK92/00036
; FILING DATE: 06-FEB-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Agriis, Cheryl H.
; REGISTRATION NUMBER: 34,086
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; REFERENCE/DOCKET NUMBER: 3396.214-US
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 212-867-0123
 ; TELEFAX: 212-867-0298
 ; INFORMATION FOR SEQ ID NO: 1:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 222 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; US-08-090-048-1

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DB	67	----	RNGTS	----	YPYGSVKSTRYFIPSGWRSGNTN	----	YDYGAIELSEPIGNTVGYF 113	
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: July 1, 2005, 21:08:25 ; Search time 90.3582 Seconds
(without alignments)
1673.692 Million cell updates/sec

Title: US-09-658-677-15

Perfect score: 2131

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Scoring table: BLOSUM62

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Searched: 1722976 seqs, 385795295 residues

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Maximum DB seq length: 2000000000

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Listing first 45 summaries

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Published Applications AA:*

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- 2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
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- 21: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
- 22: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2080	97.6	383	9	US-09-765-205-12
2	2080	97.6	383	9	US-09-909-320-261
3	2080	97.6	383	9	US-09-909-088B-261
4	2080	97.6	383	9	US-09-905-291A-261
5	2080	97.6	383	9	US-09-902-853-261
6	2080	97.6	383	9	US-09-907-824-261
7	2080	97.6	383	9	US-09-907-841-261
8	2080	97.6	383	10	US-09-904-011-261
9	2080	97.6	383	10	US-09-903-640-261
10	2080	97.6	383	10	US-09-908-093-261
11	2080	97.6	383	10	US-09-906-742-261

12	2080	97.6	383	10	US-09-906-838-261	Sequence 261, App
13	2080	97.6	383	10	US-09-907-613-261	Sequence 261, App
14	2080	97.6	383	10	US-09-907-942-261	Sequence 261, App
15	2080	97.6	383	10	US-09-904-859-261	Sequence 261, App
16	2080	97.6	383	10	US-09-903-204-261	Sequence 261, App
17	2080	97.6	383	10	US-09-904-820-261	Sequence 261, App
18	2080	97.6	383	10	US-09-904-786-261	Sequence 261, App
19	2080	97.6	383	10	US-09-906-646-261	Sequence 261, App
20	2080	97.6	383	10	US-09-906-700-261	Sequence 261, App
21	2080	97.6	383	10	US-09-903-786-261	Sequence 261, App
22	2080	97.6	383	10	US-09-902-903-261	Sequence 261, App
23	2080	97.6	383	10	US-09-903-749A-261	Sequence 261, App
24	2080	97.6	383	10	US-09-904-119-261	Sequence 261, App
25	2080	97.6	383	10	US-09-904-956-261	Sequence 261, App
26	2080	97.6	383	10	US-09-902-736-261	Sequence 261, App
27	2080	97.6	383	10	US-09-907-794-261	Sequence 261, App
28	2080	97.6	383	10	US-09-903-943-261	Sequence 261, App
29	2080	97.6	383	10	US-09-904-462-261	Sequence 261, App
30	2080	97.6	383	10	US-09-907-925-261	Sequence 261, App
31	2080	97.6	383	10	US-09-902-692-261	Sequence 261, App
32	2080	97.6	383	10	US-09-903-520-261	Sequence 261, App
33	2080	97.6	383	10	US-09-905-056-261	Sequence 261, App
34	2080	97.6	383	10	US-09-984-130-45	Sequence 45, Appl
35	2080	97.6	383	10	US-09-984-130-126	Sequence 126, App
36	2080	97.6	383	10	US-09-909-064-261	Sequence 261, App
37	2080	97.6	383	10	US-09-904-553-261	Sequence 261, App
38	2080	97.6	383	10	US-09-905-381-261	Sequence 261, App
39	2080	97.6	383	10	US-09-904-485-261	Sequence 261, App
40	2080	97.6	383	10	US-09-903-348-261	Sequence 261, App
41	2080	97.6	383	10	US-09-905-088-261	Sequence 261, App
42	2080	97.6	383	10	US-09-907-575-261	Sequence 261, App
43	2080	97.6	383	10	US-09-905-075-261	Sequence 261, App
44	2080	97.6	383	10	US-09-902-759-261	Sequence 261, App
45	2080	97.6	383	10	US-09-902-634-261	Sequence 261, App

ALIGNMENTS

RESULT 1

US-09-765-205-12
; Sequence 12, Application US/09765205
; Patent No. US20020034800A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Li
; TITLE OF INVENTION: BONE MARROW SECRETED PROTEINS AND POLYNUCLEOTIDES
; FILE REFERENCE: 1458.004/200130.449
; CURRENT APPLICATION NUMBER: US/09/765,205
; CURRENT FILING DATE: 2001-01-17
; PRIOR APPLICATION NUMBER: US/09/212,440
; PRIOR FILING DATE: 1998-12-16
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 12
; LENGTH: 383
; TYPE: PRT
; ORGANISM: human
; US-09-765-205-12

Query Match 97.6%; Score 2080; DB 9; Length 383;
Best Local Similarity 100.0%; Pred. No. 2,2e-193;
Matches 383; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 MAGIPGLLFLFLCAVQVSPYAPWKPTWPAYRLPVVLPOSTLNLAKEPFGAAKLE 60
Sequence 261, App
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Sequence 261, App
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Sequence 261, App

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RESULT 2
US-09-909-320-261
; Sequence 261, Application US/09909320
; Patent No. US20020132240A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kijavini, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/909,320
; PRIOR FILING DATE: 2002-01-04
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214

; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 261
; LENGTH: 383
; TYPE: PRT
; ORGANISM: Homo Sapien
US-09-909-320-261

Query Match 97.6%; Score 2080; DB 9; Length 383;
Best Local Similarity 100.0%; Pred. No. 2.2e-193; Mismatches 0; Indels 0; Gaps 0;
Matches 383; Conservative 0;

QY 1 MAGIPGLLFLFLFLLCAVGVQSPYSAPWKPWPAYRLPVLPQSTINLAKPFGAEAKLE 60
Db 1 MAGIPGLLFLFLFLLCAVGVQSPYSAPWKPWPAYRLPVLPQSTINLAKPFGAEAKLE 60
QY 61 VSSSCGPGCHKGTPLPPTYEEAKQYLSYETLYANGSRTETQVGIYILSSSGDGAQHRDSSG 120
Db 61 VSSSCGPGCHKGTPLPPTYEEAKQYLSYETLYANGSRTETQVGIYILSSSGDGAQHRDSSG 120
QY 121 SGKSRKRQIYGYDSRPSIFGKDFLLNYPSTSVKLSGTCTGLVAEKHVLTAHCHIDG 180
Db 121 SGKSRKRQIYGYDSRPSIFGKDFLLNYPSTSVKLSGTCTGLVAEKHVLTAHCHIDG 180
QY 181 KTYVKGTKLRVGLFKPKFKDGGRGANDSTSAMPEQMKFQWIRVKRTHVPKGIKGNAND 240
Db 181 KTYVKGTKLRVGLFKPKFKDGGRGANDSTSAMPEQMKFQWIRVKRTHVPKGIKGNAND 240
QY 241 IGMDYDVALLELKKPHKPKFKMGKIGVSPPAKQLPGGRHFGSGYDNDPRGNLVRFCVDKDE 300
Db 241 IGMDYDVALLELKKPHKPKFKMGKIGVSPPAKQLPGGRHFGSGYDNDPRGNLVRFCVDKDE 300
QY 301 TYDLLYQCCDAQPGASGSGVYVVMWKROQKWKRIIGIFSGHQWVDMNGSPQDFNVAVR 360
Db 301 TYDLLYQCCDAQPGASGSGVYVVMWKROQKWKRIIGIFSGHQWVDMNGSPQDFNVAVR 360
QY 361 ITPLKYAQICYWIKGNLYDCREG 383
Db 361 ITPLKYAQICYWIKGNLYDCREG 383

RESULT 3
US-09-909-088B-261
; Sequence 261, Application US/09909088B
; Patent No. US20020146709A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.

APPLICANT: Grimaldi, Christopher J.
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth, J.
APPLICANT: Kijavin, Ivar J.
APPLICANT: Mather, Jennie P.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: 10466-14
CURRENT APPLICATION NUMBER: US/09/909,088B
PRIOR FILING DATE: 2001-07-18
PRIOR APPLICATION NUMBER: PCT/US00/04414
PRIOR FILING DATE: 2000-02-22
PRIOR APPLICATION NUMBER: US 60/143,048
PRIOR FILING DATE: 1999-07-07
PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR FILING DATE: 1999-07-26
PRIOR APPLICATION NUMBER: US 60/146,222
PRIOR FILING DATE: 1999-07-28
PRIOR APPLICATION NUMBER: PCT/US99/20594
PRIOR FILING DATE: 1999-09-08
PRIOR APPLICATION NUMBER: PCT/US99/20944
PRIOR FILING DATE: 1999-09-13
PRIOR APPLICATION NUMBER: PCT/US99/21090
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/21547
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/23089
PRIOR FILING DATE: 1999-10-05
PRIOR APPLICATION NUMBER: PCT/US99/28214
PRIOR FILING DATE: 1999-11-29
PRIOR APPLICATION NUMBER: PCT/US99/28313
PRIOR FILING DATE: 1999-11-30
PRIOR APPLICATION NUMBER: PCT/US99/28564
PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/28565
PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/30095
PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: PCT/US99/30911
PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US99/30999
PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US00/00219
PRIOR FILING DATE: 2000-01-05
NUMBER OF SEQ ID NOS: 423
SEQ ID NO 261
LENGTH: 383
TYPE: PRT
ORGANISM: Homo Sapien
US-09-909-088B-261

Query Match 97.6%; Score 2080; DB 9; Length 383;
Best Local Similarity 100.0%; Pred. No. 2.2e-193;
Matches 383; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MAGIPGLFLPFLLCAGVGQSPSPYAPWKPWPAYRLPVVLPSTLNLAKPFGAEAKLE 60
Db 1 MAGIPGLFLPFLLCAGVGQSPSPYAPWKPWPAYRLPVVLPSTLNLAKPFGAEAKLE 60

Qy 61 VSSSCGQCHKPTLPYEAQYLSVETLYANGSTETQVGIYILSSGSGAQRHDSGS 120
Db 61 VSSSCGQCHKPTLPYEAQYLSVETLYANGSTETQVGIYILSSGSGAQRHDSGS 120

Qy 121 SGKSRKRQIYGYDSRFSIFGKDFLLNYPSTSVKLSGTCTGLTVAEKHVLTAHCHIDG 180
Db 121 SGKSRKRQIYGYDSRFSIFGKDFLLNYPSTSVKLSGTCTGLTVAEKHVLTAHCHIDG 180

Qy 181 KTYVKGTKLRVGFGLKPKFKGCGRGANDSTSAMPEOMKQWIRVKEHPKGIKGNAND 240
Db 181 KTYVKGTKLRVGFGLKPKFKGCGRGANDSTSAMPEOMKQWIRVKEHPKGIKGNAND 240

Qy 241 IGMVDYDYLLELLEKPKHKKFKMIGVSPPAKQLPGGRIHFSGYDNDPRGNLVYRFGCDVKDE 300
Db 241 IGMVDYDYLLELLEKPKHKKFKMIGVSPPAKQLPGGRIHFSGYDNDPRGNLVYRFGCDVKDE 300

Qy 301 TYDLLYQCCDAQPGASGSGVYVMKQRQOKKVERKIIGIFSGHGWYDMNGSPQDFNVAVR 360
Db 301 TYDLLYQCCDAQPGASGSGVYVMKQRQOKKVERKIIGIFSGHGWYDMNGSPQDFNVAVR 360

Qy 361 ITPLKYAQICYWIKGNLYDCREG 383
Db 361 ITPLKYAQICYWIKGNLYDCREG 383

RESULT 4
US-09-905-291A-261
Sequence 261, Application US/09905291A
Patent No. US20020160374A1
GENERAL INFORMATION:
APPLICANT: Genentech, Inc.
APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Goddard, A.
APPLICANT: Grimaldi, Christopher J.
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth, J.
APPLICANT: Kijavin, Ivar J.
APPLICANT: Mather, Jennie P.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: 10466-14
CURRENT APPLICATION NUMBER: US/09/905,291A
PRIOR FILING DATE: 2001-07-12
PRIOR APPLICATION NUMBER: PCT/US00/04414
PRIOR FILING DATE: 2000-02-22
PRIOR APPLICATION NUMBER: US 60/143,048
PRIOR FILING DATE: 1999-07-07
PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR FILING DATE: 1999-07-26
PRIOR APPLICATION NUMBER: US 60/146,222
PRIOR FILING DATE: 1999-07-28
PRIOR APPLICATION NUMBER: PCT/US99/20594
PRIOR FILING DATE: 1999-09-08
PRIOR APPLICATION NUMBER: PCT/US99/20944
PRIOR FILING DATE: 1999-09-13
PRIOR APPLICATION NUMBER: PCT/US99/21090
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/21547
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/23089
PRIOR FILING DATE: 1999-10-05
PRIOR APPLICATION NUMBER: PCT/US99/28214
PRIOR FILING DATE: 1999-11-29

QY	181	KTYYVGTQKLRVGFLLKPKFKDGGRGANDSTSAMPEQMKFQWIRVKRTHVPKGIKGNAND	240
Db	181	KTYYVGTQKLRVGFLLKPKFKDGGRGANDSTSAMPEQMKFQWIRVKRTHVPKGIKGNAND	240
QY	241	IGMDYDVALLELKKPHKKFKMKIGVSPPAKQLPGRTHFSGYDNDRPGNLVYRFFCDVKDE	300
Db	241	IGMDYDVALLELKKPHKKFKMKIGVSPPAKQLPGRTHFSGYDNDRPGNLVYRFFCDVKDE	300
QY	301	TYDLYVQCDAQPGASGSGVYVVMKRRQKQKWKERKIIIGIFSGHQWMDMNGSPQDFNVAVR	360
Db	301	TYDLYVQCDAQPGASGSGVYVVMKRRQKQKWKERKIIIGIFSGHQWMDMNGSPQDFNVAVR	360
QY	361	ITPLKYAQICYWIKGNLYDCREG	383
Db	361	ITPLKYAQICYWIKGNLYDCREG	383
RESULT 6			
US-09-907-824-261			
; Sequence 261, Application US/09907824			
; Publication No. US20020197671A1			
; GENERAL INFORMATION:			
; APPLICANT: Genentech, Inc.			
; APPLICANT: Ashkenazi, Avi			
; APPLICANT: Botstein, David			
; APPLICANT: Desnoyers, Luc			
; APPLICANT: Eaton, Dan L.			
; APPLICANT: Ferrara, Napoleone			
; APPLICANT: Filvaroff, Ellen			
; APPLICANT: Fong, Sherman			
; APPLICANT: Gao, Wei-Qiang			
; APPLICANT: Gerber, Hanspeter			
; APPLICANT: Gerritsen, Mary E.			
; APPLICANT: Goddard, A.			
; APPLICANT: Godowski, Paul J.			
; APPLICANT: Grimaldi, Christopher J.			
; APPLICANT: Gurney, Austin L.			
; APPLICANT: Hillan, Kenneth, J.			
; APPLICANT: Kljavin, Ivar J.			
; APPLICANT: Mather, Jennie P.			
; APPLICANT: Pan, James			
; APPLICANT: Paoni, Nicholas F.			
; APPLICANT: Roy, Margaret Ann			
; APPLICANT: Stewart, Timothy A.			
; APPLICANT: Tumas, Daniel			
; APPLICANT: Williams, P. Mickey			
; APPLICANT: Wood, William, I.			
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic			
; TITLE OF INVENTION: Acids Encoding the Same			
; FILE REFERENCE: 10466-14			
; CURRENT APPLICATION NUMBER: US/09/907,824			
; CURRENT FILING DATE: 2001-07-17			
; PRIOR APPLICATION NUMBER: 09/665,350			
; PRIOR FILING DATE: 2000-09-18			
; PRIOR APPLICATION NUMBER: PCT/US00/04414			
; PRIOR FILING DATE: 2000-02-22			
; PRIOR APPLICATION NUMBER: US 60/143,048			
; PRIOR FILING DATE: 1999-07-07			
; PRIOR APPLICATION NUMBER: US 60/145,698			
; PRIOR FILING DATE: 1999-07-26			
; PRIOR APPLICATION NUMBER: US 60/146,222			
; PRIOR FILING DATE: 1999-07-28			
; PRIOR APPLICATION NUMBER: PCT/US99/20594			
; PRIOR FILING DATE: 1999-09-08			
; PRIOR APPLICATION NUMBER: PCT/US99/20944			
; PRIOR FILING DATE: 1999-09-13			
; PRIOR APPLICATION NUMBER: PCT/US99/21090			
; PRIOR FILING DATE: 1999-09-15			
; PRIOR APPLICATION NUMBER: PCT/US99/21547			
; PRIOR FILING DATE: 1999-09-15			
; PRIOR APPLICATION NUMBER: PCT/US99/23089			
; PRIOR FILING DATE: 1999-10-05			
; PRIOR APPLICATION NUMBER: PCT/US99/28214			

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; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kijavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: 10466-14
; CURRENT FILING DATE: 2001-11-20
; PRIOR APPLICATION NUMBER: US/09/907,841
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 261
; LENGTH: 383
; TYPE: PRT
; ORGANISM: Homo Sapien
; US-09-907-841-261

Query Match          97.6%; Score 2080; DB 9; Length 383;
Best Local Similarity 100.0%; Pred. No. 2,2e-193;
Matches 383; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1  MAGIPGLFLLFLLCAVGQVSPYSAPWKPPTWPAAYRLPVVLPOSTLNLAKPDFGAEAKLE 60
Db      1  MAGIPGLFLLFLLCAVGQVSPYSAPWKPPTWPAAYRLPVVLPOSTLNLAKPDFGAEAKLE 60

Qy      61  VSSSCGPQCHKGTPLTYERAKQYLSYETLIYANGSRTEQVGIYILSSGDCGAQHRDSSG 120
Db      61  VSSSCGPQCHKGTPLTYERAKQYLSYETLIYANGSRTEQVGIYILSSGDCGAQHRDSSG 120

Qy      121  SGKSRKRQIYGVDSRFSGIFGKDFLNPPESTSVKLTGCTGTVAEKHVLTAACHHDG 180
Db      121  SGKSRKRQIYGVDSRFSGIFGKDFLNPPESTSVKLTGCTGTVAEKHVLTAACHHDG 180

Qy      181  KTVYVGTQKLRVGLFKPKFGKGGGRGANDSTSAMPEQMKFQWIRVVRKTRHVPKGIKNAND 240
Db      181  KTVYVGTQKLRVGLFKPKFGKGGGRGANDSTSAMPEQMKFQWIRVVRKTRHVPKGIKNAND 240

Qy      241  IGMDDYALLELKKPHKPKMKI GVSPPAKQLPGGRIFHSGYNDPRGNLVYRFDVQKE 300
Db      241  IGMDDYALLELKKPHKPKMKI GVSPPAKQLPGGRIFHSGYNDPRGNLVYRFDVQKE 300

Qy      301  TYDLLYQCCDAQPGASGSGVYVRWKKRQOQKWERKIIIGIFSGHQWDMNGSPQDFNVAVR 360
Db      301  TYDLLYQCCDAQPGASGSGVYVRWKKRQOQKWERKIIIGIFSGHQWDMNGSPQDFNVAVR 360
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Qy      361  ITPLYKQAQICYWIKNYLDREG 383
Db      361  ITPLYKQAQICYWIKNYLDREG 383

RESULT 8
US-09-904-011-261
; Sequence 261, Application US/09904011
; Publication No. US20030003530A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kijavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/904,011
; CURRENT FILING DATE: 2001-07-11
; PRIOR APPLICATION NUMBER: 09/665,350
; PRIOR FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
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/ PRIOR FILING DATE: 1999-12-20
/ PRIOR APPLICATION NUMBER: PCT/US00/00219
/ PRIOR FILING DATE: 2000-01-05
/ NUMBER OF SEQ ID NOS: 423
/ SEQ ID NO 261
/ LENGTH: 383
/ TYPE: PRT
/ ORGANISM: Homo Sapien
US-09-904-011-261

Query Match          97.6%; Score 2080; DB 10; Length 383;
Best Local Similarity 100.0%; Pred. No. 2.2e-193;
Matches 383; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAGIPGLLFLFLLCAVGVSPYSAPWKPPTWPAAYRLPVVLPSTLNLAKEPFGAEAKLE 60
DB 1 MAGIPGLLFLFLLCAVGVSPYSAPWKPPTWPAAYRLPVVLPSTLNLAKEPFGAEAKLE 60

QY 61 VSSSCGPOCHKGTPLTPTYEAKQYLSYETLYANGSRTETQVGIIYILSSSGDGAQHRDGS 120
DB 61 VSSSCGPOCHKGTPLTPTYEAKQYLSYETLYANGSRTETQVGIIYILSSSGDGAQHRDGS 120

QY 121 SGKSRKRQIYGYSRFSIFGKDFLLNYPSTSVKLTGCTGTTLVAEKHVLTAACHIDG 180
DB 121 SGKSRKRQIYGYSRFSIFGKDFLLNYPSTSVKLTGCTGTTLVAEKHVLTAACHIDG 180

QY 181 KTVVKGTKLRVGLFKPKFQDGGRGANDSTSAMPEQMKFQWIRVKTHTVPKGIKNAND 240
DB 181 KTVVKGTKLRVGLFKPKFQDGGRGANDSTSAMPEQMKFQWIRVKTHTVPKGIKNAND 240

QY 241 IGMDDYDYLLELKKPKHKKFMKIGVSPPAKQLPGGRIFHSGYDNDPRGNLVYRFDVKDE 300
DB 241 IGMDDYDYLLELKKPKHKKFMKIGVSPPAKQLPGGRIFHSGYDNDPRGNLVYRFDVKDE 300

QY 301 TYDLYQQCDAOPGASGSGVYVMMKRRQOQKWERKIIGIFSGHQWDMNGSPQDFNVAVR 360
DB 301 TYDLYQQCDAOPGASGSGVYVMMKRRQOQKWERKIIGIFSGHQWDMNGSPQDFNVAVR 360

QY 361 ITPLKYAQICYWIKGNLYDCREG 383
DB 361 ITPLKYAQICYWIKGNLYDCREG 383

RESULT 9
US-09-903-640-261
/ Sequence 261, Application US/09903640
/ Publication No. US20030017463A1
/ GENERAL INFORMATION:
/ APPLICANT: Genentech, Inc.
/ APPLICANT: Ashkenazi, Avi
/ APPLICANT: Botstein, David
/ APPLICANT: Desnoyers, Luc
/ APPLICANT: Eaton, Dan L.
/ APPLICANT: Ferrara, Napoleone
/ APPLICANT: Filvaroff, Ellen
/ APPLICANT: Fong, Sherman
/ APPLICANT: Gao, Wei-Qiang
/ APPLICANT: Gerber, Hanspeter
/ APPLICANT: Gerritsen, Mary E.
/ APPLICANT: Goddard, A.
/ APPLICANT: Godowski, Paul J.
/ APPLICANT: Grimaldi, Christopher J.
/ APPLICANT: Hillan, Kenneth, J.
/ APPLICANT: Kljavin, Ivar J.
/ APPLICANT: Mather, Jennie P.
/ APPLICANT: Pan, James
/ APPLICANT: Paoni, Nicholas F.
/ APPLICANT: Stewart, Timothy A.
/ APPLICANT: Tumas, Daniel
/ APPLICANT: Williams, P. Mickey
/ APPLICANT: Wood, William, I.

/ TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
/ TITLE OF INVENTION: Acids Encoding the Same
/ FILE REFERENCE: 10466-14
/ CURRENT APPLICATION NUMBER: US/09/903,640
/ CURRENT FILING DATE: 2001-07-11
/ PRIOR APPLICATION NUMBER: 09/665,350
/ PRIOR FILING DATE: 2000-09-18
/ NUMBER OF SEQ ID NOS: 423
/ SEQ ID NO 261
/ LENGTH: 383
/ TYPE: PRT
/ ORGANISM: Homo Sapien
US-09-903-640-261

Query Match          97.6%; Score 2080; DB 10; Length 383;
Best Local Similarity 100.0%; Pred. No. 2.2e-193;
Matches 383; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAGIPGLLFLFLLCAVGVSPYSAPWKPPTWPAAYRLPVVLPSTLNLAKEPFGAEAKLE 60
DB 1 MAGIPGLLFLFLLCAVGVSPYSAPWKPPTWPAAYRLPVVLPSTLNLAKEPFGAEAKLE 60

QY 61 VSSSCGPOCHKGTPLTPTYEAKQYLSYETLYANGSRTETQVGIIYILSSSGDGAQHRDGS 120
DB 61 VSSSCGPOCHKGTPLTPTYEAKQYLSYETLYANGSRTETQVGIIYILSSSGDGAQHRDGS 120

QY 121 SGKSRKRQIYGYSRFSIFGKDFLLNYPSTSVKLTGCTGTTLVAEKHVLTAACHIDG 180
DB 121 SGKSRKRQIYGYSRFSIFGKDFLLNYPSTSVKLTGCTGTTLVAEKHVLTAACHIDG 180

QY 181 KTVVKGTKLRVGLFKPKFQDGGRGANDSTSAMPEQMKFQWIRVKTHTVPKGIKNAND 240
DB 181 KTVVKGTKLRVGLFKPKFQDGGRGANDSTSAMPEQMKFQWIRVKTHTVPKGIKNAND 240

QY 241 IGMDDYDYLLELKKPKHKKFMKIGVSPPAKQLPGGRIFHSGYDNDPRGNLVYRFDVKDE 300
DB 241 IGMDDYDYLLELKKPKHKKFMKIGVSPPAKQLPGGRIFHSGYDNDPRGNLVYRFDVKDE 300

QY 301 TYDLYQQCDAOPGASGSGVYVMMKRRQOQKWERKIIGIFSGHQWDMNGSPQDFNVAVR 360
DB 301 TYDLYQQCDAOPGASGSGVYVMMKRRQOQKWERKIIGIFSGHQWDMNGSPQDFNVAVR 360

QY 361 ITPLKYAQICYWIKGNLYDCREG 383
DB 361 ITPLKYAQICYWIKGNLYDCREG 383

RESULT 10
US-09-908-093-261
/ Sequence 261, Application US/09908093
/ Publication No. US20030017498A1
/ GENERAL INFORMATION:
/ APPLICANT: Genentech, Inc.
/ APPLICANT: Ashkenazi, Avi
/ APPLICANT: Botstein, David
/ APPLICANT: Desnoyers, Luc
/ APPLICANT: Eaton, Dan L.
/ APPLICANT: Ferrara, Napoleone
/ APPLICANT: Filvaroff, Ellen
/ APPLICANT: Fong, Sherman
/ APPLICANT: Gao, Wei-Qiang
/ APPLICANT: Gerber, Hanspeter
/ APPLICANT: Gerritsen, Mary E.
/ APPLICANT: Goddard, A.
/ APPLICANT: Godowski, Paul J.
/ APPLICANT: Grimaldi, Christopher J.
/ APPLICANT: Gurney, Austin L.
/ APPLICANT: Hillan, Kenneth, J.
/ APPLICANT: Kljavin, Ivar J.
/ APPLICANT: Mather, Jennie P.
/ APPLICANT: Pan, James
/ APPLICANT: Paoni, Nicholas F.
/ APPLICANT: Roy, Margaret Ann
```

APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: 10466-14
CURRENT APPLICATION NUMBER: US/09/908,093
CURRENT FILING DATE: 2001-07-17
PRIOR APPLICATION NUMBER: 09/665,350
PRIOR FILING DATE: 2000-09-18
PRIOR APPLICATION NUMBER: PCT/US00/04414
PRIOR FILING DATE: 2000-02-22
PRIOR APPLICATION NUMBER: US 60/143,048
PRIOR FILING DATE: 1999-07-07
PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR FILING DATE: 1999-07-26
PRIOR APPLICATION NUMBER: US 60/146,222
PRIOR FILING DATE: 1999-07-28
PRIOR APPLICATION NUMBER: PCT/US99/20594
PRIOR FILING DATE: 1999-09-08
PRIOR APPLICATION NUMBER: PCT/US99/20944
PRIOR FILING DATE: 1999-09-13
PRIOR APPLICATION NUMBER: PCT/US99/21090
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/21547
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/23089
PRIOR FILING DATE: 1999-10-05
PRIOR APPLICATION NUMBER: PCT/US99/28214
PRIOR FILING DATE: 1999-11-29
PRIOR APPLICATION NUMBER: PCT/US99/28313
PRIOR FILING DATE: 1999-11-30
PRIOR APPLICATION NUMBER: PCT/US99/28564
PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/28565
PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/30095
PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: PCT/US99/30911
PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US99/30999
PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US00/00219
PRIOR FILING DATE: 2000-01-05
NUMBER OF SEQ ID NOS: 423
SEQ ID NO 261
LENGTH: 383
TYPE: PRT
ORGANISM: Homo Sapien
US-09-908-093-261

Query Match 97.6%; Score 2080; DB 10; Length 383;
Best Local Similarity 100.0%; Pred. No. 2,2e-193;
Matches 383; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAGIPGLFLFLLCAVGVSPYSAPWKPWTWPAYRLPVVLPOSTLNLAKEPFGAEAKLE 60
Db 1 MAGIPGLFLFLLCAVGVSPYSAPWKPWTWPAYRLPVVLPOSTLNLAKEPFGAEAKLE 60

QY 61 VSSSCGPGCHKGTPPTYPEAKOYLSETLYANGSRTETQVGIYILSSSGDGAQHRDGS 120
Db 61 VSSSCGPGCHKGTPPTYPEAKOYLSETLYANGSRTETQVGIYILSSSGDGAQHRDGS 120

QY 121 SGKSRKROIYGVDSRFSFGKDFLNYPSTSVKLSCTGTLVAEKHVLTAACHIDG 180
Db 121 SGKSRKROIYGVDSRFSFGKDFLNYPSTSVKLSCTGTLVAEKHVLTAACHIDG 180

QY 181 KTVVKGTQKLRVGFLLPKPKFGDGRGANDSTSAMPEQMKFQWIRVKRTHVPKGIKNAND 240
Db 181 KTVVKGTQKLRVGFLLPKPKFGDGRGANDSTSAMPEQMKFQWIRVKRTHVPKGIKNAND 240

QY 241 IGMDDYALLELKKPHKRFMKIGVSPPAKQLPGGRIHFSGYDNDRPGNLVYRFDVKDE 300

Db 241 IGMDDYALLELKKPHKRFMKIGVSPPAKQLPGGRIHFSGYDNDRPGNLVYRFDVKDE 300
QY 301 TYDLLYQCCDAQGASGSGVYVMMKRCQOKWERKIIGIFSGHQWYDMNGSPQDFNVAVR 360
Db 301 TYDLLYQCCDAQGASGSGVYVMMKRCQOKWERKIIGIFSGHQWYDMNGSPQDFNVAVR 360
QY 361 ITPKYAQICYWIKGNYLDCREG 383
Db 361 ITPKYAQICYWIKGNYLDCREG 383

RESULT 11
US-09-906-742-261
Sequence 261, Application US/09906742
Publication No. US20030023054A1
GENERAL INFORMATION:
APPLICANT: Genentech, Inc.
APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, A.
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, Christopher J.
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth, J.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Mather, Jennie P.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: 10466-14
CURRENT APPLICATION NUMBER: US/09/906,742
CURRENT FILING DATE: 2001-07-16
PRIOR APPLICATION NUMBER: 09/665,350
PRIOR FILING DATE: 2000-09-18
PRIOR APPLICATION NUMBER: PCT/US00/04414
PRIOR FILING DATE: 2000-02-22
PRIOR APPLICATION NUMBER: US 60/143,048
PRIOR FILING DATE: 1999-07-07
PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR FILING DATE: 1999-07-26
PRIOR APPLICATION NUMBER: US 60/146,222
PRIOR FILING DATE: 1999-07-28
PRIOR APPLICATION NUMBER: PCT/US99/20594
PRIOR FILING DATE: 1999-09-08
PRIOR APPLICATION NUMBER: PCT/US99/20944
PRIOR FILING DATE: 1999-09-13
PRIOR APPLICATION NUMBER: PCT/US99/21090
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/21547
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/23089
PRIOR FILING DATE: 1999-10-05
PRIOR APPLICATION NUMBER: PCT/US99/28214
PRIOR FILING DATE: 1999-11-29
PRIOR APPLICATION NUMBER: PCT/US99/28313
PRIOR FILING DATE: 1999-11-30
PRIOR APPLICATION NUMBER: PCT/US99/28564
PRIOR FILING DATE: 1999-12-02

;; PRIOR APPLICATION NUMBER: PCT/US99/28565
;; PRIOR FILING DATE: 1999-12-02
;; PRIOR APPLICATION NUMBER: PCT/US99/30095
;; PRIOR FILING DATE: 1999-12-16
;; PRIOR APPLICATION NUMBER: PCT/US99/30911
;; PRIOR FILING DATE: 1999-12-20
;; PRIOR APPLICATION NUMBER: PCT/US99/30999
;; PRIOR FILING DATE: 1999-12-20
;; PRIOR APPLICATION NUMBER: PCT/US00/00219
;; PRIOR FILING DATE: 2000-01-05
;; NUMBER OF SEQ ID NOS: 423
;; SEQ ID NO 261
;; LENGTH: 383
;; TYPE: PRT
;; ORGANISM: Homo Sapien
US-09-906-742-261

Query Match 97.6%; Score 2080; DB 10; Length 383;
Best Local Similarity 100.0%; Pred. No. 2.2e-193;
Matches 383; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAGIPGLLFLFLLCAVGVSPYSAPWKPWPAYRLPVVLPQSTLNLAKEPFGAEAKLE 60
Db 1 MAGIPGLLFLFLLCAVGVSPYSAPWKPWPAYRLPVVLPQSTLNLAKEPFGAEAKLE 60

QY 61 VSSSCGPGQCHKGTPLTPEEAKQYLSYETLYANGSRSTETQVGIYILSSSGDGAQHRDGS 120
Db 61 VSSSCGPGQCHKGTPLTPEEAKQYLSYETLYANGSRSTETQVGIYILSSSGDGAQHRDGS 120

QY 121 SGKSRKRQIYGYDSRFSIFGKDFLNYPFSTSVKLSGTCTGLTVAEKHVLTAACHIDG 180
Db 121 SGKSRKRQIYGYDSRFSIFGKDFLNYPFSTSVKLSGTCTGLTVAEKHVLTAACHIDG 180

QY 181 KTYVGTQKLRVGLFKPKFGKGGRGANDSTSAMPEQMKFQWIRVKTTHPKGWIKNAND 240
Db 181 KTYVGTQKLRVGLFKPKFGKGGRGANDSTSAMPEQMKFQWIRVKTTHPKGWIKNAND 240

QY 241 IGHVDYALLEKPKHKKFEMKIGVSPAPKQLPGGRHIFSGYNDPRGNLVYRFDVKDE 300
Db 241 IGHVDYALLEKPKHKKFEMKIGVSPAPKQLPGGRHIFSGYNDPRGNLVYRFDVKDE 300

QY 301 TYDLLYQQCDAQSGSGVYVVMKRWQKQKWKIIGIFSGHWDVMDNGSPQDFNVAVR 360
Db 301 TYDLLYQQCDAQSGSGVYVVMKRWQKQKWKIIGIFSGHWDVMDNGSPQDFNVAVR 360

QY 361 ITPLKVAQICYNKGNLYDCREG 383
Db 361 ITPLKVAQICYNKGNLYDCREG 383

RESULT 12
US-09-906-838-261
; Sequence 261, Application US/09906838
; Publication No. US20030027143A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnovers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kijavini, Ivar J.
; APPLICANT: Mather, Jennie P.

;; APPLICANT: Pan, James
;; APPLICANT: Paoni, Nicholas F.
;; APPLICANT: Roy, Margaret Ann
;; APPLICANT: Stewart, Timothy A.
;; APPLICANT: Tumas, Daniel
;; APPLICANT: Williams, P. Mickey
;; APPLICANT: Wood, William, I.
;; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;; TITLE OF INVENTION: Acids Encoding the Same
;; FILE REFERENCE: 10466-14
;; CURRENT APPLICATION NUMBER: US/09/906,838
;; CURRENT FILING DATE: 2001-07-16
;; PRIOR APPLICATION NUMBER: 09/665,350
;; PRIOR FILING DATE: 2000-09-18
;; PRIOR APPLICATION NUMBER: PCT/US00/04414
;; PRIOR FILING DATE: 2000-02-22
;; PRIOR APPLICATION NUMBER: US 60/143,048
;; PRIOR FILING DATE: 1999-07-07
;; PRIOR APPLICATION NUMBER: US 60/145,698
;; PRIOR FILING DATE: 1999-07-26
;; PRIOR APPLICATION NUMBER: US 60/146,222
;; PRIOR FILING DATE: 1999-07-28
;; PRIOR APPLICATION NUMBER: PCT/US99/20594
;; PRIOR FILING DATE: 1999-09-08
;; PRIOR APPLICATION NUMBER: PCT/US99/20944
;; PRIOR FILING DATE: 1999-09-13
;; PRIOR APPLICATION NUMBER: PCT/US99/21090
;; PRIOR FILING DATE: 1999-09-15
;; PRIOR APPLICATION NUMBER: PCT/US99/21547
;; PRIOR FILING DATE: 1999-09-15
;; PRIOR APPLICATION NUMBER: PCT/US99/23089
;; PRIOR FILING DATE: 1999-10-05
;; PRIOR APPLICATION NUMBER: PCT/US99/28214
;; PRIOR FILING DATE: 1999-11-29
;; PRIOR APPLICATION NUMBER: PCT/US99/28313
;; PRIOR FILING DATE: 1999-11-30
;; PRIOR APPLICATION NUMBER: PCT/US99/28564
;; PRIOR FILING DATE: 1999-12-02
;; PRIOR APPLICATION NUMBER: PCT/US99/28565
;; PRIOR FILING DATE: 1999-12-02
;; PRIOR APPLICATION NUMBER: PCT/US99/30095
;; PRIOR FILING DATE: 1999-12-16
;; PRIOR APPLICATION NUMBER: PCT/US99/30911
;; PRIOR FILING DATE: 1999-12-20
;; PRIOR APPLICATION NUMBER: PCT/US99/30999
;; PRIOR FILING DATE: 1999-12-20
;; PRIOR APPLICATION NUMBER: PCT/US00/00219
;; PRIOR FILING DATE: 2000-01-05
;; NUMBER OF SEQ ID NOS: 423
;; SEQ ID NO 261
;; LENGTH: 383
;; TYPE: PRT
;; ORGANISM: Homo Sapien
US-09-906-838-261

Query Match 97.6%; Score 2080; DB 10; Length 383;
Best Local Similarity 100.0%; Pred. No. 2.2e-193;
Matches 383; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAGIPGLLFLFLLCAVGVSPYSAPWKPWPAYRLPVVLPQSTLNLAKEPFGAEAKLE 60
Db 1 MAGIPGLLFLFLLCAVGVSPYSAPWKPWPAYRLPVVLPQSTLNLAKEPFGAEAKLE 60

QY 61 VSSSCGPGQCHKGTPLTPEEAKQYLSYETLYANGSRSTETQVGIYILSSSGDGAQHRDGS 120
Db 61 VSSSCGPGQCHKGTPLTPEEAKQYLSYETLYANGSRSTETQVGIYILSSSGDGAQHRDGS 120

QY 121 SGKSRKRQIYGYDSRFSIFGKDFLNYPFSTSVKLSGTCTGLTVAEKHVLTAACHIDG 180
Db 121 SGKSRKRQIYGYDSRFSIFGKDFLNYPFSTSVKLSGTCTGLTVAEKHVLTAACHIDG 180

QY 181 KTYVGTQKLRVGLFKPKFGKGGRGANDSTSAMPEQMKFQWIRVKTTHPKGWIKNAND 240
Db 181 KTYVGTQKLRVGLFKPKFGKGGRGANDSTSAMPEQMKFQWIRVKTTHPKGWIKNAND 240

Db 181 KTYVGTOKLRVGLFKPKFKDGGGANDSTSAMPEQMKFQWIRVKRTHVPKGIKGNAND 240
QY 241 IGMDDYDYLLELKKPKFKFKMGKIGVSPPAKQLFGGRHFSGYDNDPRGNLVYRFCDDVDE 300
Db 241 IGMDDYDYLLELKKPKFKFKMGKIGVSPPAKQLFGGRHFSGYDNDPRGNLVYRFCDDVDE 300
QY 301 TYDLLYQQCDAOPGASGSGVYVVMWKRQOQKWERKIIGIFSGHQWDMNGSPQDFNVAVR 360
Db 301 TYDLLYQQCDAOPGASGSGVYVVMWKRQOQKWERKIIGIFSGHQWDMNGSPQDFNVAVR 360
QY 361 ITPLKYAQICYWIKGNLYDCREG 383
Db 361 ITPLKYAQICYWIKGNLYDCREG 383

RESULT 13

US-09-907-613-261
; Sequence 261, Application US/09907613
; Publication No. US20030027145A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kijavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/907,613
; CURRENT FILING DATE: 2001-07-17
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564

; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 261
; LENGTH: 383
; TYPE: PRT
; ORGANISM: Homo Sapien
US-09-907-613-261
Query Match 97.6%; Score 2080; DB 10; Length 383;
Best Local Similarity 100.0%; Pred. No. 2.2e-193;
Matches 383; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MAGIPQLLFLFLCAVGVSPYAPWKPTWPAYRLPVVLPQSTLNLAKPDFGAERKLE 60
Db 1 MAGIPQLLFLFLCAVGVSPYAPWKPTWPAYRLPVVLPQSTLNLAKPDFGAERKLE 60
QY 61 VSSSCGPQCHKGTPLPTYEAAKQYLSYETLYANGSRTTETQVGIYILSSSGDGAQHRDGS 120
Db 61 VSSSCGPQCHKGTPLPTYEAAKQYLSYETLYANGSRTTETQVGIYILSSSGDGAQHRDGS 120
QY 121 SKSRRKQIYGYDSRFSIFGKDFLLNYPFSTSVKLSCTCTTLVAEKHVLTAACHIDG 180
Db 121 SKSRRKQIYGYDSRFSIFGKDFLLNYPFSTSVKLSCTCTTLVAEKHVLTAACHIDG 180
QY 181 KTYVGTOKLRVGLFKPKFKDGGGANDSTSAMPEQMKFQWIRVKRTHVPKGIKGNAND 240
Db 181 KTYVGTOKLRVGLFKPKFKDGGGANDSTSAMPEQMKFQWIRVKRTHVPKGIKGNAND 240
QY 241 IGMDDYDYLLELKKPKFKFKMGKIGVSPPAKQLFGGRHFSGYDNDPRGNLVYRFCDDVDE 300
Db 241 IGMDDYDYLLELKKPKFKFKMGKIGVSPPAKQLFGGRHFSGYDNDPRGNLVYRFCDDVDE 300
QY 301 TYDLLYQQCDAOPGASGSGVYVVMWKRQOQKWERKIIGIFSGHQWDMNGSPQDFNVAVR 360
Db 301 TYDLLYQQCDAOPGASGSGVYVVMWKRQOQKWERKIIGIFSGHQWDMNGSPQDFNVAVR 360
QY 361 ITPLKYAQICYWIKGNLYDCREG 383
Db 361 ITPLKYAQICYWIKGNLYDCREG 383
RESULT 14
US-09-907-942-261
; Sequence 261, Application US/09907942
; Publication No. US20030027146A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kijavin, Ivar J.

APPLICANT: Mather, Jennie P.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: 10466-14
CURRENT APPLICATION NUMBER: US/09/907,942
CURRENT FILING DATE: 2002-01-22
PRIOR APPLICATION NUMBER: PCT/US00/04414
PRIOR FILING DATE: 2000-02-22
PRIOR FILING DATE: US 60/143,048
PRIOR FILING DATE: 1999-07-07
PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR FILING DATE: 1999-07-26
PRIOR APPLICATION NUMBER: US 60/146,222
PRIOR FILING DATE: 1999-07-28
PRIOR APPLICATION NUMBER: PCT/US99/20594
PRIOR FILING DATE: 1999-09-08
PRIOR APPLICATION NUMBER: PCT/US99/20944
PRIOR FILING DATE: 1999-09-13
PRIOR APPLICATION NUMBER: PCT/US99/21090
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/21547
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/23089
PRIOR FILING DATE: 1999-10-05
PRIOR APPLICATION NUMBER: PCT/US99/28214
PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/28565
PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/30095
PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: PCT/US99/30911
PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US99/30999
PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US00/00219
PRIOR FILING DATE: 2000-01-05
NUMBER OF SEQ ID NOS: 423
SEQ ID NO 261
LENGTH: 383
TYPE: PRT
ORGANISM: Homo Sapien
US-09-907-942-261

Query Match 97.6%; Score 2080; DB 10; Length 383;
Best Local Similarity 100.0%; Pred. No. 2,2e-193;
Matches 383; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 MAGIPGLFLFLLCVAGQVSPYAPWKPWPAYRLPVVLPSTLNLAQPDFAEAKLE 60
1 MAGIPGLFLFLLCVAGQVSPYAPWKPWPAYRLPVVLPSTLNLAQPDFAEAKLE 60
61 VSSSCGPGQCHKGTPLTPEAKQYLYETLYANGSRTEQVGIIYILSSSGDGAQRHDSGS 120
61 VSSSCGPGQCHKGTPLTPEAKQYLYETLYANGSRTEQVGIIYILSSSGDGAQRHDSGS 120
121 SGKSRKRQIYGVDSRFSIFGKDFLLNYPSTSVKLSCTGCTGLVAEKVLTAAHCHIDG 180
121 SGKSRKRQIYGVDSRFSIFGKDFLLNYPSTSVKLSCTGCTGLVAEKVLTAAHCHIDG 180
181 KTVVGTQKLRVGLFKPKDGGGRGANDSTSAMPEQMKFQWIRVKKRTHVPKGIKGNAND 240
181 KTVVGTQKLRVGLFKPKDGGGRGANDSTSAMPEQMKFQWIRVKKRTHVPKGIKGNAND 240

QY 241 IGMDYDYLLELKKPHKRFMKIGVSPPAKOLPGGRIHESGYDNDPRGNLVYRFDVKDE 300
DB 241 IGMDYDYLLELKKPHKRFMKIGVSPPAKOLPGGRIHESGYDNDPRGNLVYRFDVKDE 300
QY 301 TYDLYLQQCDAPGASGSGVYVVMWKRQQQKWKRIIGIFSGHQWVDMNGSPQDFNVAVR 360
DB 301 TYDLYLQQCDAPGASGSGVYVVMWKRQQQKWKRIIGIFSGHQWVDMNGSPQDFNVAVR 360
QY 361 ITPLKYAQICYWIKGNLYDCREG 383
DB 361 ITPLKYAQICYWIKGNLYDCREG 383

RESULT 15

US-09-904-859-261
Sequence 261, Application US/09904859
Publication No. US20030036060A1
GENERAL INFORMATION:
APPLICANT: Genentech, Inc.
APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, A.
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, Christopher J.
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth, J.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Mather, Jennie P.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: 10466-14
CURRENT APPLICATION NUMBER: US/09/904,859
CURRENT FILING DATE: 2001-07-12
PRIOR APPLICATION NUMBER: 09/665,350
PRIOR FILING DATE: 2000-09-18
PRIOR APPLICATION NUMBER: PCT/US00/04414
PRIOR FILING DATE: 2000-02-22
PRIOR APPLICATION NUMBER: US 60/143,048
PRIOR FILING DATE: 1999-07-07
PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR FILING DATE: 1999-07-26
PRIOR APPLICATION NUMBER: US 60/146,222
PRIOR FILING DATE: 1999-07-28
PRIOR APPLICATION NUMBER: PCT/US99/20594
PRIOR FILING DATE: 1999-09-08
PRIOR APPLICATION NUMBER: PCT/US99/20944
PRIOR FILING DATE: 1999-09-13
PRIOR APPLICATION NUMBER: PCT/US99/21090
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/21547
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/23089
PRIOR FILING DATE: 1999-10-05
PRIOR APPLICATION NUMBER: PCT/US99/28214
PRIOR FILING DATE: 1999-11-29
PRIOR APPLICATION NUMBER: PCT/US99/28313
PRIOR FILING DATE: 1999-11-30

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; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 261
; LENGTH: 383
; TYPE: PRT
; ORGANISM: Homo Sapien
US-09-904-859-261

Query Match      97.6%; Score 2080; DB 10; Length 383;
Best Local Similarity 100.0%; Pred. No. 2.2e-193;
Matches 383; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1  MAGIPGLFLLFLLCAVGVSPYSAPWKPWTWPAYRLPVVLPQSTLNLAKPDPFGAEAKLE 60
Db      1  MAGIPGLFLLFLLCAVGVSPYSAPWKPWTWPAYRLPVVLPQSTLNLAKPDPFGAEAKLE 60

Qy      61  VSSSCGPOCHKGTPLTYEAKQYLSYETLYANGSRTEQVGIYIILSSGQGAQHRDGS 120
Db      61  VSSSCGPOCHKGTPLTYEAKQYLSYETLYANGSRTEQVGIYIILSSGQGAQHRDGS 120

Qy      121  SGKSRKRQIYGYDSRFSIFGKDFLLNYPFSTSVKLSCTGTTLVAEKHVLTAAHCIHDG 180
Db      121  SGKSRKRQIYGYDSRFSIFGKDFLLNYPFSTSVKLSCTGTTLVAEKHVLTAAHCIHDG 180

Qy      181  KTVVKTQKLRVGFLLKPKFKDGGGANDSTSAMPEQMKQWIRVKRTHVPKGIKGNAND 240
Db      181  KTVVKTQKLRVGFLLKPKFKDGGGANDSTSAMPEQMKQWIRVKRTHVPKGIKGNAND 240

Qy      241  IGMDYDVALLELKKPKRPFMKIGVSPPAKQLPGGRIHFSGYDNDPRGNLVYRFCVDKDE 300
Db      241  IGMDYDVALLELKKPKRPFMKIGVSPPAKQLPGGRIHFSGYDNDPRGNLVYRFCVDKDE 300

Qy      301  TYDLLYQQCDAQPGASGSGYVVRMVKRQQQKWERKIIGIFSGHQWYDMNGSPQDFNVAVR 360
Db      301  TYDLLYQQCDAQPGASGSGYVVRMVKRQQQKWERKIIGIFSGHQWYDMNGSPQDFNVAVR 360

Qy      361  ITPKYAQICYWIKGNLYDCREG 383
Db      361  ITPKYAQICYWIKGNLYDCREG 383
```

Search completed: July 1, 2005, 21:32:17
Job time : 91.3582 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 1, 2005, 20:54:23 ; Search time 20.826 seconds
(without alignments)
1811.048 Million cell updates/sec

Title: US-09-658-677-15

Perfect score: 2131

Sequence: 1 MAGIPGLFLFLFLCAVGO.....IKGNVLDRCRGDTVPPGNS 392

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: PIR 79.*

2: PIR2.*

3: PIR3.*

4: PIR4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	194	9.1	316	2 A45134	endopeptidase (EC
2	135.5	6.4	313	2 A35122	metalloproteinase
3	131	6.1	218	2 E97915	choline binding pr
4	120.5	5.7	482	1 EXRT	coagulation factor
5	119	5.6	269	2 A26823	pancreatic elastas
6	117	5.5	522	2 T29767	hypothetical prote
7	115.5	5.4	269	2 B26823	pancreatic elastas
8	115.5	5.4	271	2 A25528	pancreatic elastas
9	115	5.4	258	4 S70439	pancreatic elastas
10	115	5.4	267	4 A56615	probable pancreati
11	114.5	5.4	238	1 TRW5Y	trypsin-like prote
12	114.5	5.4	285	2 C95045	choline binding pr
13	114	5.3	246	1 DBHU	complement factor
14	113	5.3	266	1 ELPG	pancreatic elastas
15	113	5.3	266	1 ELRT1	pancreatic elastas
16	112.5	5.3	259	1 TRSMG	trypsin (EC 3.4.21
17	112.5	5.3	273	2 E85765	hypothetical prote
18	112.5	5.3	273	2 H64915	putative protease
19	111.5	5.2	488	1 EXHU	coagulation factor
20	111	5.2	761	2 JC5759	brain-specific ser
21	110	5.2	269	2 C26823	pancreatic elastas
22	110	5.2	492	1 EXBO	coagulation factor
23	110	5.2	1582	2 T15308	hypothetical prote
24	109.5	5.1	405	2 T35117	probable secreted
25	109	5.1	278	2 AH0282	probable peptidas
26	108	5.1	583	2 A29154	complement factor
27	108	5.1	786	1 A47547	serine proteinase
28	108	5.1	1047	2 A55617	masquerade precurs
29	107.5	5.0	236	2 A28566	T-cell suppressor

30	107.5	5.0	686	1 A59271	Ra-reactive factor
31	105	4.9	274	2 S40004	trypsin-related pr
32	103.5	4.9	271	1 ELRT2	pancreatic elastas
33	103.5	4.9	416	1 KFBO	coagulation factor
34	102.5	4.8	1238	2 T34929	hypothetical prote
35	100	4.7	272	2 JC4170	trypsin-like prote
36	100	4.7	855	2 JC7731	membrane-bound arg
37	98.5	4.6	267	2 S40006	trypsin (EC 3.4.21
38	98	4.6	548	2 D82175	probable trypsin V
39	98	4.6	624	2 T02289	probable polygalac
40	97.5	4.6	409	2 T35118	probable secreted
41	97.5	4.6	452	1 A30351	coagulation factor
42	97.5	4.6	747	2 I51579	complement factor
43	97	4.6	1019	2 A38738	coagulation factor
44	96.5	4.5	259	2 S68424	allergen Der f III
45	96.5	4.5	275	2 I46712	factor IX - rabbit

ALIGNMENTS

RESULT 1

A45134

endopeptidase (EC 3.4.-.-), glutamate-specific - Bacillus licheniformis

C;Species: Bacillus licheniformis

C;Date: 10-Jun-1993 #sequence_revision 18-Nov-1994 #text_change 16-Aug-2004

C;Accession: A45134; S23078

R;Kakudo, S.; Kikuchi, N.; Kitadokoro, K.; Fujiwara, T.; Nakamura, E.; Okamoto, H.; Shin, J. Biol. Chem. 267, 23782-23788, 1992

A;Title: Purification, characterization, cloning, and expression of a glutamic acid-speci

A;Reference number: A45134; MUID:93054737; PMID:1429718

A;Accession: A45134

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-316 <RAK>

A;Cross-references: UNIPROT:P80057; GB:D10060; NID:g216263; PIDN:BAA00949.1; PID:d100141

A;Experimental source: ATCC 14580

A;Note: sequence extracted from NCBI backbone (NCBIN:118784, NCBIPI:118785)

R;Svendsen, I.; Breddam, K.

Eur. J. Biochem. 204, 165-171, 1992

A;Title: Isolation and amino acid sequence of a glutamic acid specific endopeptidase from

A;Reference number: S23078; MUID:92155199; PMID:1346764

A;Accession: S23078

A;Status: preliminary

A;Molecule type: protein

A;Residues: 95-316 <SVS>

C;Superfamily: Glutamyl endopeptidase, V8 type

C;Keywords: hydrolase

Query Match 9.1%; Score 194; DB 2; Length 316;

Best Local Similarity 24.0%; Pred. No. 2e-08;

Matches 79; Conservative 43; Mismatches 143; Indels 64; Gaps 15;

QY 63 SSCGPCQCHGTPL---PTVEEAKQVLSYETLYANGSRTEQTQVGIYILSSSGDGAQHRDSG 119

Db 28 AQAPSPH--TPVSSDPSTV-KAETSVDYD-----NIKSDQYGLYSKAFGTGKVNTEKE 79

QY 120 SSGKSRKRQIYGYDSRFSIFGKDFLLN-----YPFSTSVKLST---GCTGLVAEKHV 170

Db 80 KAEKSPAKAPY---SIKSVIGSDDRTRVTNTTAYPYRAIVHISSTSGCTGWMIGPKTV 136

QY 171 LTAHCHIHGKT-YVKGTKLRVGFLLKPKFKDGGGRANDSTSAMPEQMKQWIRVKRTHV 229

Db 137 ATAGHCIIYDTSSGSPAGTATVSPG-----RNGTS-----YYPGYSVKSTRFYI 178

QY 230 PKGWIKGNANDIGMDYDYLLELKKPKRKFMIKIGVSPPAKQLPGGRIHSGYDNDNRPGN 289

Db 179 PSQWRSGNTN-----YDYGAIELSEFIGNTVGVFGYSYTTSSLVGTTVTSIGPGDKTAG 233

QY 290 LVYRFCD--VKDETYDLLYQQCDAPQASGSGVYVVRMKRQQQKWERKII---GIFSGH 343

Db 234 TQWQHSPTAISYTKLYQYAM-DTYGQSGSPVFEQSSSRSTNCSPCLAVHTNGVYGG- 291

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QY 344 QWDMNGSPQDFNVAVRITPLKVAQICYW 372
Db 292 -----SSYNRGTRITKEVFDNLTNW 311

RESULT 2
A:Title: metalloproteinase (EC 3.4.17.1) mpr precursor, extracellular - Bacillus subtilis
C:Species: Bacillus subtilis
C:Date: 27-Jul-1990 #sequence_revision 27-Jul-1990 #text_change 16-Aug-2004
C:Accession: A35122; I40010; A69660
R:Sloma, A.; Rudolph, C.F.; Rufo Jr., G.A.; Sullivan, B.J.; Theriault, K.A.; Ally, D.; F
J. Bacteriol. 172, 1024-1029, 1990
A:Title: Gene encoding a novel extracellular metalloprotease in Bacillus subtilis.
A:Reference number: A35122; MUID:90130256; PMID:2105291
A:Accession: A35122
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-313 <SLO>
A:Cross-references: UNIPROT:P39790; GB:L10505; NID:G143209; PIDN:AAA22604.1; PID:G143210
R:Smith, H.; de Jong, A.; Bron, S.; Venema, G.
Gene 70, 351-361, 1988
A:Title: Characterization of signal-sequence-coding regions selected from the Bacillus s
A:Reference number: I39994; MUID:89108019; PMID:3145906
A:Accession: I40010
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-60, 65, 'L', 67, 'S', 69, 'AQA' <RES>
A:Cross-references: GB:M22916; NID:G143701; PIDN:AAA22832.1; PID:G143702
R:Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Bertel
C.; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Ch
A.; Ehrlich, S.D.; Emmeron, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.
Nature 390, 249-256, 1997
A:Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Gallen
iech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F.
Koetter, P.; Konigstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois,
A:Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maueel
Y, M.; Ogawa, K.; Ogilwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelle
Rieger, M.; Rivolta, C.; Roche, E.; Roche, M.; Sadate, Y.; Sato, T.; Scanlon,
A:Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Seron
akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiyama
T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, K
A:Authors: Yoshikawa, H.F.; Zumbstein, E.; Yoshikawa, H.; Danchin, A.
A:Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.
A:Reference number: A69580; MUID:98044033; PMID:9384377
A:Accession: A69660
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-313 <KUN>
A:Cross-references: GB:Z99105; GB:AL009126; NID:G2632457; PIDN:CAB12018.1; PID:G1182176;
A:Experimental source: strain 168
C:Genetics:
A:Superfamily: Glutamyl endopeptidase, V8 type
C:Keywords: hydrolase

Query Match 6.4%; Score 135.5; DB 2; Length 313;
Best Local Similarity 22.2%; Pred. No. 0.0014;
Matches 77; Conservative 39; Mismatches 121; Indels 111; Gaps 17;

QY 72 GTPLPYVEAKQVLSVETLYANGSRTRTQVGIYILSSGD--CAQHRDSSGSSKSRKQ 129
Db 29 GVPKAAENPQTSVNSGTREADTKNQ-----SKADQVSAPYEGTGKTSK----- 75

QY 130 IYGYDSRF-----STFGKD-----FLNLYPFSVSKLST-----GCTGTL 164
Db 76 LYGGQTELEKNIGTLOFSSIIIGTDERISSTTSFPYRATVQLSIKYPNVTSYTGCTGL 135

QY 165 VAEKHVLTAAHCIIH-----DGKTYVKGQKLRVGLPKFKDGGRGAND 208
Db 136 VNPNVTVTAGHCYVSDHGWASTITAAPGRNGSSYPYGY----- 175

QY 209 STSAMPEQMKFQIRVKRTHVPGWIKGN---ANDIGMDYDVALLELKPFPKFKMKIGV 265
```

```
Db 176 -SCTMFYSVK-GWTESKOTNYDYGAIKLNGSPGNTVGM-YGYRTTNSSP-----VGL 225
QY 266 SPPAKQLPGGRIHFSGYDNDPRGNLVYRFDVKDEYDLLYQOCDAQPGASGSGVTVRMW 325
Db 226 SSSVVGFPDCKTFGTGWSDTKPIR-----SAETYKLTYY-TTDTYGCQSGSPVY---- 272

QY 326 KRQQQKWKERKIIGIFSGHQMVDMNGSPQDFNVAVRITPLKVAQICYW 372
Db 273 -RNYSDTGQTALAIHT-----NGG-SSYNLGTRVNDVFNNIQYW 310

RESULT 3
E97915
A:Title: choline binding protein G, truncation [imported] - Streptococcus pneumoniae (strain R6)
C:Species: Streptococcus pneumoniae
C:Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 09-Jul-2004
C:Accession: E97915
R:Hoskins, J.A.; Alborn Jr., W.; Arnold, J.; Blaszcak, L.; Bargett, S.; DeHoff, B.S.; E
e, R.; LeBlanc, D.J.; Lee, L.N.; Lefkowitz, E.J.; Lu, J.; Matsushima, P.; McAhren, S.; M
Y, P.; Sun, P.M.; Winkler, M.E.
J. Bacteriol. 183, 5709-5717, 2001
A:Authors: Yang, Y.; Young-Bellido, M.; Zhao, G.; Zook, C.; Baltz, R.H.; Jaskunas, S.R.;
A:Title: Genome of the Bacterium Streptococcus pneumoniae Strain R6.
A:Reference number: A97872; MUID:21429245; PMID:11544234
A:Accession: E97915
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-218 <KUR>
A:Cross-references: UNIPROT:Q8DR41; GB:AE007317; PIDN:AAK99153.1; PID:G15457907; GSPDB:G
C:Genetics:
A:Gene: cbpG-truncation

Query Match 6.1%; Score 131; DB 2; Length 218;
Best Local Similarity 24.2%; Pred. No. 0.0021;
Matches 59; Conservative 30; Mismatches 87; Indels 68; Gaps 10;

QY 143 DFLNYPFSTSVKLSGCTG-----TLVAEKHVLTAACHIDHGKTYVKGTOK 189
Db 5 DNTLQVPYSTSAWLSKYVGVADGMNVEGRSGSANFKDNLVITAAH-----NYYR---- 54

QY 190 LRVGFLPKPKFKDGGRGAND---STSAMPEQMKFQIRVKRTHVPGWIKGNANDIGMDYD 246
Db 55 -----HDYKEADIIYVLPVAVSPSQELFKYKVEKRYLKEFRNLNSKD-AREYD 103

QY 247 YALLELKPFPKFKFKMGKIVGSPPAKOLPGGRIHFSGYDNDPRGNLVYRF-----CDVKDE 300
Db 104 LALLILEKPIGAKLTGLTGLPTSQKNTLGTITVITGYPS-----YNFKIHQMYTDKKQV 156

QY 301 TYD---LLYQQCDAQPGASGSGVYVYRMWKROQKWKRIIGIFSGHQMVDMNGSPQDFNV 357
Db 157 LSDDGMFLDYQVDTLEGSSGSTVY-----DASHRVVGVHT-----LGDGANQINS 201

QY 358 AVRI 361
Db 202 AVKL 205

RESULT 4
EXPT
A:Title: coagulation factor Xa (EC 3.4.21.6) precursor - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 31-Jan-1995 #sequence_revision 07-Feb-1997 #text_change 09-Jul-2004
C:Accession: S49075; J04670; P0191; P0190; I62745
R:Stanton, C.; Ross, P.; Hutson, S.; Wallin, R.
Thromb. Res. 80, 63-73, 1995
A:Title: Evidence for competition between vitamin K-dependent clotting factors for intrac
A:Reference number: A59498; MUID:96093366; PMID:8578539
A:Accession: S49075
A:Molecule type: mRNA
A:Residues: 1-482 <STAL>
A:Cross-references: UNIPROT:Q63207; EMBL:X79807; NID:G506600; PIDN:CAA56202.1; PID:G50660
A:Note: submitted to the EMBL Data Library, June 1994
```

A>Note: neither the complete nucleic acid sequence nor the complete translation are shown

R; Stanton, C.; Ross, R.P.; Hutson, S.; Wallin, R.
Gene 169, 269-273, 1996
A>Title: Processing and expression of rat and human clotting factor-X-encoding cDNAs.
A;Reference number: JC4670; MUID:96194815; PMID:8647460
A;Accession: JC4670
A;Molecule type: mRNA
A;Residues: 1-482 <STA2>
A;Cross-references: EMBL:X79807; NID:g506600; PIDN:CAA56202.1; PID:g506601
A;Experimental source: Cos-1 cell
R; Enryoji, K.; Miyazaki, K.; Kato, H.
J. Biochem. 109, 890-898, 1991
A;Title: Characterization of rat factors X and Xa: demonstration of factor Xa in rat plasma
A;Reference number: PS0190; MUID:92041742; PMID:1718949
A;Accession: PS0191
A;Molecule type: protein
A;Residues: 41-58,'X','60-65 <ENJ1>
A;Accession: PS0190
A;Molecule type: protein
A;Residues: 183-186,'X','188-207 <ENJ2>
R; Murakawa, M.; Okamura, T.; Kamura, T.; Kuroiwa, M.; Harada, M.; Niho, Y.
Eur. J. Haematol. 52, 162-168, 1994
A;Title: Analysis of the partial nucleotide sequences and deduced primary structures of
A;Reference number: I46196; MUID:942222160; PMID:8168596
A;Accession: I62745
A>Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 295-383,'G','385-455 <MUR>
A;Cross-references: GB:D21215; NID:g415309; PIDN:BAA04756.1; PID:g455396
C;Function:
A;Description: catalyzes the proteolytic activation of prothrombin to thrombin in the presence of Factor V
A;Pathway: blood coagulation
C;Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homology
C;Keywords: beta-hydroxyaspartic acid; blood coagulation; calcium binding; carboxyglutamic acid
F;1-23/Domain: signal sequence #status predicted <SIG>
F;24-40/Domain: propetide #status predicted <PRO>
F;25-84/Domain: Gla domain homology <GLA>
F;41-179/Product: coagulation factor X light chain #status predicted <LCH>
F;90-121/Domain: EGF homology <EG1>
F;129-164/Domain: EGF homology <EG2>
F;183-482/Product: coagulation factor X heavy chain #status predicted <HCH>
F;183-231/Domain: activation peptide #status predicted <APT>
F;232-482/Product: coagulation factor Xa heavy chain #status predicted <ACT>
F;232-460/Domain: trypsin homology <TRY>
F;46,47,54,56,59,60,65,66,69,72,79/Modified site: gamma-carboxyglutamic acid (Glu) #stat
F;57-62,90-101,95-110,112-121,129-140,136-149,151-164,172-340,238-243,259-275,388-402,41
F;103/Modified site: erythro-beta-hydroxyaspartic acid (Asp) #status predicted
F;108/Binding site: carbohydrate (Asn) (covalent) #status experimental
F;208/Binding site: carbohydrate (Thr) (covalent) #status predicted
F;218/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;231-232/Cleavage site: Arg-11e (coagulation factor IXa, coagulation factor VIIa) #stat
F;274,320,417/Active site: His, Asp, Ser #status predicted

Query Match 5.7%; Score 120.5; DB 1; Length 482;
Best Local Similarity 32.3%; Pred.No. 0.041;
Matches 31; Conservative 17; Mismatches 23; Indels 25; Gaps 4;

OY 160 CYTTLVAEKHLTAACHIDKGVVKGTKLRVGFLKPFKDGGGRANDSTAMPQMKP 219
||| : ||||||| : | : ||| : ||| :
DB 259 CGGTILNEFYLTAAHCLHQAKGF-----KVRYVDLTLEQEDGGMVHE-VDMIIKHNF 312
||| : ||||||| : | : ||| : ||| :
OY 220 QWIRVKRTVPKGIWKGNANDIGMDYDALLELKPK 255
||| : ||| : ||| : ||| : ||| :
DB 313 Q-----RDVT-----DFDIWLRLKTP 329
||| : ||| : ||| : ||| : ||| :

RESULT 5
A26823
N;Alternate names: pancreatic elastase II (EC 3.4.21.71) precursor - pig
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 16-Aug-1988 #sequence revision 16-Aug-1988 #text_change 09-Jul-2004
C;Accession: A26823

R:Kawashima, I.; Tani, T.; Shimoda, K.; Takiguchi, Y.
DNA 6, 163-172, 1987
A:Title: Characterization of pancreatic elastase II cDNAs: two elastase II mRNAs are expressed from the same gene in the rat pancreas
A:Reference number: A90958; MUID:87217962; PMID:3646943
A:Accession: A26823
A:Molecule type: mRNA
A:Residues: 1-269 <KAW>
A:Cross-references: UNIPROT:P08419; GB:M16651; NID:gl64441; PIDN:AAA31027.1; PID:gl64442
C:Superfamily: trypsin; trypsin homology
C:Keywords: hydrolase; serine proteinase
F:1-16/Domain: signal sequence #status predicted <SIG>
F:17-28/Domain: propeptide #status predicted <PRO>
F:29-269/Product: elastase II #status predicted <MAT>
F:29-262/Domain: trypsin homology <TRY>
F:73,121,216/Active site: His, Asp, Ser #status predicted

Query Match 5.6%; Score 119; DB 2; Length 269;
Best Local Similarity 27.5%; Pred. No. 0.027;
Matches 60; Conservative 28; Mismatches 64; Indels 66; Gaps 14;

QY 128 RQIVGVDSRSPFSGKDFLLNYPFSTSVKL-STG-----CTGTTLVAEKHVLTAACHIDGK 181
DB 28 RVVGGEDARPN-----SWPQVSLQYDSSGQWRHTCGTILVDQSFWLTAACHISSR 79
QY 182 TY--VKGTKQLRVGFLKPKFKDGGRGANDSTSAMPEQMKFQWIRVXKTHVPGKWIKNAN 239
DB 80 TYRVVLGRHSL-----STNEPGLA-----VKVSKLVVHQDW--NSN 114
QY 240 DIGMDYDYLLELKKP-HKRFKFMKIGVSPPAQK-LPG-----GRIHFGSYDND--R 286
DB 115 QLSNGNDIALLLKASPSVSLTDKIQLGCLPAAAGTILPNNNYCVYVGTGWRGLQTNGASPDILQ 174
QY 287 PGNLVYRFPDVKDRTYDLYOCCDAOPGASGSGVYVRM 324
DB 175 QGQLL-----VVD-----YATC-SKPGWGSTVKTNM 200

RESULT 6
T29767
hypothetical protein ZC581.6 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C:Accession: T29767
R:Waterston, B.; Gattung, S.; Le, T.T.
submitted to the EMBL Data Library, May 1997
A:Description: The sequence of C. elegans cosmid ZC581.
A:Reference number: Z20682
A:Accession: T29767
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-522 <WAT>
A:Cross-references: UNIPROT:O01771; EMBL:AF003134; PIDN:AAB54144.1; GSPDB:GN00019; CESP:Z102.1
A:Experimental source: strain Bristol N2; clone ZC581
C:Genetics:
A:Gene: CESP:ZC581.6
A:Map position: 1
A:Introns: 36/2; 138/3; 234/2; 311/1; 331/1; 421/1; 470/2

Query Match 5.5%; Score 117; DB 2; Length 522;
Best Local Similarity 20.4%; Pred. No. 0.089;
Matches 95; Conservative 56; Mismatches 153; Indels 162; Gaps 21;

QY 29 KPTWPAVRLPVVLQPSLTNLAKDPFGAEAKLEVSS--CGPQCHKGTPLPTVEEAKQ-- 83
DB 26 KPSNKASSAPSLRKSSNPNKGTVARSVKSPVPSAIPASTVQKEVPPEVEKKKEEK 85
QY 84 -----YLSYETLYANGSRRTETQVGIYILSSSGDGAQHRDSSGSKSRKRQIYGYDSRF 137
DB 86 PENQKXELAEKKU---DRTQDDCKEYKAESALGVVWKEDKAPAKWDDGYEDFGPCEP 141
QY 138 SIFGKD-----FLNYPFSTSV-----KLTGCTGTTLVAEK 168
DB 142 PFLFKTILEMILYMLRIPFSKAVYNGNRDASQSEAPWSVFTLYSKDQSATTTCTGTIVSPR 201

QY 169 HVLTAHCI-----HDGK-----TYVKGTKL--RVGFLKPKFGDGRGA 206
 Db 202 HILLIATCFAGQNRDGSWNLIEDTFRSNCCKDDYVITNDFEFLKRVFELSNK-----253
 QY 207 NDSTSAMPEQMKFQWIRVKEVTPKWKIGNANDIGMDY---DYALLEL-----252
 Db 254 -KGISRYPEKITILVHACTRT-----ANRTKKIPQYYTDDFAIVHLYEELTFSSNVQ 305
 QY 253 -----KKPKHR---KFMKIGVSPPAKQLPGRGIRHFGSYDNDRLPNLVY-----292
 Db 306 SVCVADETPNDKLSLEYFGFLNPPSD-----INQNGVDN--TGQLRYEKIEVFRSH 357
 QY 293 -----RFGDVKDEYD-----LLYQOCDAQ-----PGASGSGVYVMKROQKWE 333
 Db 358 PMEIFYFQARDITDKTVACVSVSLKILILNKTOASLNISLKGDSGGGAIDV-----KGK 411
 QY 334 RKLIIGIFS-----GHQVDMNGSPQDFNVAVRITPLKYAQIC 370
 Db 412 KTIIGVLSQTSCKRRGGNETMELYSVGFYKNQI-----CKYTGIC 453
 RESULT 7
 B26823
 A:Title: Characterization of pancreatic elastase II cDNAs: two elastase II mRNAs are ex
 A:Reference number: A90958; MUID:87217962; PMID:3646943
 A:Accession: B26823
 A:Molecule type: mRNA
 A:Residues: 1-269 <RAW>
 A:Cross-references: UNIPROT:P08217; GB:M16652; NID:g182057; PIDN:AAAS2380.1; PID:g182058
 R:Fletcher, T.S.; Shen, W.F.; Largman, C.
 Biochemistry 26, 7256-7261, 1987
 A:Title: Primary structure of human pancreatic elastase 2 determined by sequence analysi
 A:Reference number: A27432; MUID:88107669; PMID:3427074
 A:Accession: A27432
 A:Molecule type: mRNA
 A:Residues: 1-269 <FILE>
 A:Cross-references: GB:M16631; NID:g182022; PIDN:AAAS2374.1; PID:g182023
 R:Shirasu, Y.; Yoshida, H.; Matsuki, S.; Takemura, K.; Ikeda, N.; Shimada, Y.; Ozawa, T.
 J. Biochem. 102, 1555-1563, 1987
 A:Title: Molecular cloning and expression in Escherichia coli of a cDNA encoding human p
 A:Reference number: A41431; MUID:88198076; PMID:2834346
 A:Accession: A41431
 A:Molecule type: mRNA
 A:Residues: 1-201,'V',203-269 <SHI>
 A:Cross-references: GB:D00236; NID:g219619; PIDN:BAA00165.1; PID:g219620
 A:Note: the authors translated the codon GTG for residue 202 as Cys
 R:Moulard, M.; Michon, T.; Kerfelec, B.; Chapus, C.
 FEBS Lett. 261, 179-183, 1990
 A:Title: Further studies on the human pancreatic binary complexes involving procarboxype
 A:Reference number: S08253; MUID:90169111; PMID:2307232
 A:Accession: S34491
 A:Molecule type: protein
 A:Residues: 'X',18-50 <MOU>
 C:Genetics:
 A:Gene: GDB:ELAL1
 A:Cross-references: GDB:119866; OMIM:130120
 A:Map position: 12pter-12qter
 C:Superfamily: trypsin; trypsin homology
 C:Keywords: hydrolase; pancreas; serine proteinase
 F:1-16/Domain: signal sequence #status predicted <SIG>
 F:17-28/Domain: propeptide #status predicted <PRO>
 F:29-269/Product: pancreatic elastase IIA #status predicted <MAT>
 F:29-262/Domain: trypsin homology <TRY>
 F:73,121,216/Active site: His, Asp, Ser #status predicted
 Query Match 5.4%; Score 115.5; DB 2; Length 269;

Best Local Similarity 28.6%; Pred. No. 0.052;
 Matches 50; Conservative 21; Mismatches 51; Indels 53; Gaps 11;
 QY 147 NYPFSTSVKLSGTG-----CTGTLVAEKHVLTAACHIDGKTYVKGTKLQKRVGFLKPKF 200
 Db 39 SNFWQVSLQSSNGKWHYTCGSLTANSWLVTAACHISSRTY-----RVGL-----85
 QY 201 DGGRG-----ANDSTSAMPEQMKFQWIRVKEVTPKWKIGNANDIGMDYDYALLELKKP- 255
 Db 86 --GRNLYVAESGSLA-----VSVSKIYVHKDW---NSNQISKGNIDIALKLANPV 131
 QY 256 HKRKPMKIGVSPPAKQ-LPG-----GRHFSGYDND--RPGNLV---YRFC 295
 Db 132 SLTDKIQLACLPAGTILPNNYPCVVTGMRLOTNGAVPVLQGGRLLVVDYATC 186
 RESULT 8
 A25528
 A:Title: Sequence organisation and transcriptional regulation of the mouse elastase II ar
 C:Species: Mus musculus (house mouse)
 C:Date: 30-Jun-1988 #sequence_revision 30-Jun-1988 #text_change 09-Jul-2004
 C:Accession: A25528
 R:Stevenson, B.J.; Hagenbuechle, O.; Wellauer, P.K.
 Nucleic Acids Res. 14, 8307-8330, 1986
 A:Title: Sequence organisation and transcriptional regulation of the mouse elastase II ar
 A:Reference number: A93646; MUID:87066713; PMID:3641189
 A:Accession: A25528
 A:Molecule type: mRNA
 A:Residues: 1-271 <STE>
 A:Cross-references: UNIPROT:P05208; GB:X04573; NID:g50825; PIDN:CAA28242.1; PID:g50826
 C:Superfamily: trypsin; trypsin homology
 C:Keywords: hydrolase; serine proteinase
 F:1-30/Domain: signal sequence #status predicted <SIG>
 F:31-271/Product: pancreatic elastase II #status predicted <MAT>
 F:31-264/Domain: trypsin homology <TRY>
 F:75,123,218/Active site: His, Asp, Ser #status predicted
 Query Match 5.4%; Score 115.5; DB 2; Length 271;
 Best Local Similarity 25.0%; Pred. No. 0.053;
 Matches 67; Conservative 38; Mismatches 80; Indels 83; Gaps 18;
 QY 148 YPFSTSVK-LSTG-----CTGTLVAEKHVLTAACHIDGKTY--VKGTKLQKRVGFLKPKF 199
 Db 42 WPMQVSLQVLSGRWRHNGCGSLVANNWVLTAAHCLSNYQTYRVLLGAHSL-----92
 QY 200 KDGGRGANDSTSAMPEQMKFQWIRVKEVTPKWKIGNANDIGMDYDYALLELKKP-HKR 258
 Db 93 --SNFGAGSAA-----VQVSKLVVHQRW---NSQVNGVDIALIKLASPTVLS 136
 QY 259 KPMKIGVSPPAKQ-LPGGRI-HFGY-----DNDRLPNLV---YRFC-----295
 Db 137 KNIQIACLPAGTILPNNYPCVVTGMRLOTNGSPDTLRQGRLLVVDYATCSSASWMS 196
 QY 296 DYKDETY-----DLLYQOCDAQPGASGSGVYVMKROQKWKERKIGIFSGHQWVDMNGS 351
 Db 197 SYKSNMVCAGGSGVTSNCN---GDSGGPLNCASNGQ---WQ--VHGIVSFGSSLGCN-Y 247
 QY 352 PDFNVAVRITPLKYAQICYKWKGNVLD 379
 Db 248 PRKPSVFRVS-----NYID 262
 RESULT 9
 S70439
 A:Title: Genomic organization of the human homologue of the rat pancreatic elastase I ger
 A:Reference number: A56615; MUID:92338395; PMID:1633328
 A:Accession: S70439
 C:Species: Homo sapiens (man)
 C:Date: 03-Aug-1998 #sequence_revision 03-Aug-1998 #text_change 28-Apr-2003
 C:Accession: S70439
 R:Kawashima, I.; Tani, T.; Mita-Honjo, K.; Shimoda-Takano, K.; Ohmine, T.; Furukawa, H.;
 DNA Seq. 2, 303-312, 1992
 A:Title: Genomic organization of the human homologue of the rat pancreatic elastase I ger
 A:Reference number: A56615; MUID:92338395; PMID:1633328
 A:Accession: S70439

RESULT 13

DBHU
Complement factor D (EC 3.4.21.46) precursor [validated] - human (fragment)
N;Alternate names: adipsin; C3 convertase activator
C;Species: Homo sapiens (man)
C;Date: 28-Aug-1985 #sequence_revision 31-Dec-1992 #text_change 09-Jul-2004
C;Accession: A40197; A00936; A60571; S66645
R;White, R.T.; Damm, D.; Hancock, N.; Rosen, B.S.; Lowell, B.B.; Usher, P.; Plier, J.S.; J. Biol. Chem. 267, 9210-9213, 1992
A;Title: Human adipsin is identical to complement factor D and is expressed at high level
A;Reference number: A40197; MUID:92250520; PMID:1374388
A;Accession: A40197
A;Molecule type: mRNA
A;Residues: 1-246 <WHI>
A;Cross-references: UNIPROT:P00746; GB:M84526
R;Niemann, M.A.; Bhowm, A.S.; Bennett, J.C.; Volanakis, J.E.
Biochemistry 23, 2482-2486, 1984
A;Title: Amino acid sequence of human D of the alternative complement pathway.
A;Reference number: A00936; MUID:85000441; PMID:6383466
A;Accession: A00936
A;Molecule type: protein
A;Residues: 19-44, 'G', 46-51, 'Q', 53-75, 'TH', 78, 'P', 80-83, 'XXXITIE', 90-172, 86-91, 185-235, 'R';
A;Note: a few residues were assigned from the previously published sequence of Reid et al.
R;Miyata, T.; Oda, O.; Inagi, R.; Sugiyama, S.; Miyama, A.; Maeda, K.; Nakashima, I.; Y. Mol. Immunol. 27, 637-644, 1990
A;Title: Molecular and functional identification and purification of complement component D.
A;Reference number: A60571; MUID:90370044; PMID:2395435
A;Accession: A60571
A;Molecule type: protein
A;Residues: 19-20, 'XX', 23-27, 'XX', 30-31, 'XX', 34, 'X', 36-40 <MIY>
R;Balke, N.; Holzkamp, U.; Hoerl, W.H.; Tschesche, H.
FEBS Lett. 371, 300-302, 1995
A;Title: Inhibition of degradation of human polymorphonuclear leukocytes by complement D.
A;Reference number: S66645; MUID:96013156; PMID:7556615
A;Accession: S66645
A;Status: preliminary
A;Molecule type: protein
A;Residues: 19-44, 'C', 46-48 <BAL>
C;Comment: Factor D cleaves factor B when the latter is complexed with factor C3b, active site:
A;Gene: GDB:DF
A;Cross-references: GDB:132645; OMIM:134350
A;Map position: Xpter-Xqter
C;Superfamily: trypsin; trypsin homology
C;Keywords: complement alternate pathway; hydrolase; plasma; serine proteinase
F;1-18/Domain: signal sequence #status predicted <SIG>
F;19-246/Product: complement factor D (fragment) #status experimental <MAT>
F;19-241/Domain: complement factor D (fragment) #status experimental <MAT>
F;44-60,141-207,172-188,197-222/bisulfide bonds: #status predicted
F;59,105,201/Active site: His, Asp, Ser #status predicted

Query Match 5.3%; Score 114; DB 1; Length 246;
Best Local Similarity 28.4%; Pred. No. 0.062;
Matches 44; Conservative 20; Mismatches 43; Indels 48; Gaps 9;

QY 149 PFSTSVKLSGTG--CTGTLVAEKHVLTAACI--DGKTVYKGTQKLRVGFLLPKPKDGG 203
DB 31 PYMASVOLNGAHLACGVLVAERWLSAAHCLDAADGKQVQL-----72
QY 204 RGNADSTSAMPEQMKQWIRVKTTHVPKGIKGNANDIGMDYDVALLELKKPHKPKMKI 263
DB 73 LGAHSLSQPEPSKRLVDVLR-----VP-----HPDSQPDTHDHLQLLQSE-----RA 117
QY 264 GYSPPAKQLPGGRIHPSGYDND--RPNGLVRFCDV 297
DB 118 TLGPAVRPLPWQRV-----DRDVAPGL-----CDV 143

RESULT 14

ELPG
pancreatic elastase (EC 3.4.21.36) I precursor - pig
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 24-Apr-1984 #sequence_revision 30-Sep-1990 #text_change 09-Jul-2004

C;Accession: JS0013; A26777; A10061; A00959
R;Shirasu, Y.; Yoshida, H.; Mikayama, T.; Matsuki, S.; Tanaka, J.I.; Ikenaga, H.
J. Biochem. 99, 1707-1712, 1986
A;Title: Isolation and expression in Escherichia coli of a cDNA clone encoding porcine pA
A;Reference number: A92005; MUID:86304235; PMID:3528137
A;Accession: JS0013
A;Molecule type: mRNA
A;Residues: 1-266 <SHI>
A;Cross-references: UNIPROT:P00772; GB:X04036; GB:D00070; GB:N00070; PIDN:gl941; PIDN:CAA;
R;Tani, T.; Kawashima, I.; Furukawa, H.; Ohmine, T.; Takiguchi, Y.
J. Biochem. 101, 591-599, 1987
A;Title: Characterization of a silent gene for human pancreatic elastase I: structure of
A;Reference number: A26777; MUID:87250343; PMID:3648024
A;Accession: A26777
A;Molecule type: mRNA
A;Residues: 1-125, 'G', 127-183, 'L', 185-266 <TAN>
A;Cross-references: GB:D00160; NID:g217683; PIDN:BAQA00118.1; PID:g217684
A;Note: the authors translated the codon GGG for residue 58 as Gln, GGC for residue 126 &
R;Shotton, D.M.; Hartley, B.S.
Biochem. J. 131, 643-675, 1973
A;Title: Evidence for the amino acid sequence of porcine pancreatic elastase.
A;Reference number: A90267; MUID:73229121; PMID:4578945
A;Accession: A10061
A;Molecule type: protein
A;Residues: 27-91, 'N', 93-203, 'N', 205-266 <SHO>
R;Shotton, D.M.; Hartley, B.S.
Nature 225, 811-816, 1970
A;Title: Three-dimensional structure of tosyl-elastase.
A;Reference number: A93160; MUID:70114044; PMID:5415110
A;Contents: annotation; X-ray crystallography, 3.5 angstroms; active site
C;Superfamily: trypsin; trypsin homology
C;Keywords: hydrolase; pancreas; serine proteinase; zymogen
F;1-16/Domain: signal sequence #status predicted <SIG>
F;17-26/Domain: activation peptide #status predicted <APT>
F;27-266/Product: elastase I #status experimental <MAT>
F;27-259/Domain: trypsin homology <TRY>
F;56-72,153-220,184-200,210-240/bisulfide bonds: #status experimental
F;71,119,214/Active site: His, Asp, Ser #status experimental

Query Match 5.3%; Score 113; DB 1; Length 266;
Best Local Similarity 27.3%; Pred. No. 0.083;
Matches 36; Conservative 21; Mismatches 41; Indels 34; Gaps 6;

QY 147 NYPFSTSVKLSGTG-----CTGTLVAEKHVLTAACIHDGKTY--VKGPKLRVGFLLPKPK 198
DB 37 SPSQISLQYRSQSSWAHTCGGTLIRQNNWMTAAACVDRELTFRVVVGHNL-----88
QY 199 FKDGGGRANDTSAMPEQMKQWIRVKTTHVPKGIKGNANDIGMDYDVALLEL-KKPHK 257
DB 89 -----NQNDGPE-----QYGVGVQIVVHPYW---NTDDVAAGYDIALRLAQSVTL 131

QY 258 RKFMKIGVSPPA 269
DB 132 NSYVLGVLPRA 143

RESULT 15
ELRT1
pancreatic elastase (EC 3.4.21.36) I precursor - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 18-Aug-1982 #sequence_revision 18-Aug-1982 #text_change 09-Jul-2004
C;Accession: A00960; A20534
R;MacDonald, R.J.; Swift, G.H.; Quinto, C.; Swain, W.; Picot, R.L.; Nikovits, W.; Rutter;
Biochemistry 21, 1453-1463, 1982
A;Title: Primary structure of two distinct rat pancreatic preproelastases determined by
A;Reference number: A00960; MUID:82182967; PMID:6918221
A;Accession: A00960
A;Molecule type: mRNA
A;Residues: 1-266 <MAC>
A;Cross-references: UNIPROT:P00773; GB:V01234; NID:G56088; PIDN:CAA24544.1; PID:g56089
R;Largman, C.
Biochemistry 22, 3763-3770, 1983
A;Title: Isolation and characterization of rat pancreatic elastase.

Search completed: July 1, 2005, 21:09:19
Job time : 21.826 secs

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OM protein - protein search, using sw model

Run on: July 1, 2005, 20:53:37 ; Search time 92.7095 Seconds
(without alignments)
2165.204 Million cell updates/sec

Title: US-09-658-677-15

Perfect score: 2131

Sequence: 1 MAGIPGLFLPFLCAVGQ.....IKGNVLDREGDVRPPGSN 392

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Uniprot 03:*

1: uniprot_sprot:*

2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2080	97.6	383	1 PS23 HUMAN	O95084 homo sapien
2	1903	89.3	383	2 O6AY61	O6ay61 rattus norv
3	1888.5	88.6	382	1 PS23 MOUSE	O9d6x6 mus musculus
4	1882.5	88.3	382	2 O8BZS4	O8bz84 mus musculus
5	1042	48.9	413	2 O9BQF6	O9bqp6 homo sapien
6	1041	48.9	413	2 O8N320	O8n320 homo sapien
7	1016.5	47.7	409	2 O8COF9	O8cof9 mus musculus
8	1014.5	47.6	418	2 O6GML6	O6gm16 brachydanio
9	1011.5	47.5	409	2 O8C0L5	O8c0d6 mus musculus
10	1005.5	47.2	409	2 O8C0D6	O8c0d6 mus musculus
11	194	9.1	316	1 GSEP BACLI	P80057 bacillus li
12	194	9.1	316	2 O65NR6	O65nr6 bacillus li
13	188	8.8	450	2 O71VE5	O71ve5 listeria mo
14	178.5	8.4	384	2 O98G17	O98g17 rhizobium l
15	158	7.4	271	2 O987W6	O987w6 rhizobium l
16	142.5	6.7	358	2 O931E7	O931e7 staphylococ
17	141.5	6.6	321	2 O7NGB4	O7ngb4 gloeobacter
18	138.5	6.5	323	2 O73D54	O73d54 bacillus ce
19	135.5	6.4	313	1 MPR BACSU	P19790 bacillus su
20	133.5	6.3	799	2 O6PF94	O6pf94 mus musculus
21	133.5	6.3	811	1 TMS6 MOUSE	O9dbi0 mus musculus
22	132.5	6.2	290	2 O81HL5	O81hl5 bacillus ce
23	131	6.1	218	2 O8DR41	O8dr41 streptococc
24	131	6.1	267	2 O6DGM4	O6dgw4 brachydanio
25	129.5	6.1	303	2 O9EXR9	O9exr9 bacillus in
26	129	6.1	286	2 O6AZC0	O6azc0 brachydanio
27	129	6.1	469	2 O9GMD9	O9gmd9 ornithorhyn
28	127.5	6.0	1322	2 O9NAT0	O9nat0 anopheles g
29	126.5	5.9	678	2 O9JJS8	O9jjs8 rattus norv
30	124.5	5.8	1234	2 O7PIQ7	O7piq7 anopheles g
31	124.5	5.8	1322	2 O7PNR7	O7pnr7 anopheles g

32	124.5	5.8	1322	2	O9NJS5	O9nje5 anopheles g
33	124	5.8	266	1	EL1 BOVIN	O28153 bos taurus
34	124	5.8	266	2	O46644	O46644 macaca fasc
35	123.5	5.8	339	2	O9QX91	O9qx91 rattus norv
36	123.5	5.8	366	2	O9QX85	O9qx85 rattus norv
37	123.5	5.8	541	2	O9QX90	O9qx90 rattus norv
38	123.5	5.8	623	2	O9QJF3	O9qjfp3 rattus norv
39	123.5	5.8	643	2	O9QX84	O9qx84 rattus norv
40	122	5.7	259	2	O9XY61	O9xy61 ctenocephal
41	122	5.7	376	1	FA10_HOPST	P83370 hoplocephal
42	122	5.7	449	2	O9VDDU8	O9vdus drosophila
43	121.5	5.7	490	1	FA10_RABIT	O19045 oryctolagus
44	121	5.7	745	2	O9QWF9	O9owf9 triakis scy
45	121	5.7	1059	2	O7Z411	O7z411 homo sapien

ALIGNMENTS

RESULT 1
PS23_HUMAN STANDARD; PRT; 383 AA.
AC O95084;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Serine protease 23 precursor (EC 3.4.21.-) (Putative secreted protein
DE ZSIG13) (UNQ270/PRO307).
GN Name=PRSS23; Synonyms=ZSIG13;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RC SEQUENCE FROM N.A.
RP TISSUE=Umbilical vein;
RA Li X., Tedder T.F.;
RT "A novel serine protease from human umbilical vein endothelial
RT cells.";
RL Submitted (JUL-1997) to the EMBL/GenBank/DBJ databases.
RN [2]
RC SEQUENCE FROM N.A.
RP Sheppard P., Blumberg H., Jelinek L., Foster D., O'Hara P.;
RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.
RN [3]
RC SEQUENCE FROM N.A.
RP TISSUE=Uterus;
RA Wiemann S., Weil B., Wellenreuther R., Gassenhuber J., Glassel S.,
Ansoerge W., Boecker M., Bloecker H., Bauersachs S., Blum H.,
Lauber J., Duetherhoff A., Beyer A., Koehrer K., Strack N.,
Mewes H.-W., Ottenwaelder B., Obermaier B., Tampe J., Heubner D.,
Wambutt R., Korn B., Klein M., Poustka A.;
RT "Towards a catalog of human genes and proteins: sequencing and
RT analysis of 500 novel complete protein coding human cDNAs.";
RL Genome Res. 11:422-435(2001).
RN [4]
RC SEQUENCE FROM N.A.
RP MEDLINE=22887296; PubMed=12975309; DOI=10.1101/gr.1293003;
RA Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D., Brush J.,
Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,
Eaton D., Foster J., Grimaldi C., Gu Q., Hase P.E., Heldens S.,
Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,
Lewis L., Liao D., Mark M., Robbie E., Sanchez C., Schoenfeld J.,
Seshagiri S., Simmons L., Smith V., Singh J., Stinson J., Vagts A.,
Vandlen R., Watanabe C., Wleand D., Woods K., Xie M.-H., Yansura D.,
Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I.,
Godowski P., Gray A.;
RT "The secreted protein discovery initiative (SPDI), a large-scale
RT effort to identify novel human secreted and transmembrane proteins: a
RT bioinformatics assessment.";
RL Genome Res. 13:2265-2270(2003).
RN [5]

DR InterPro: IPR001314; Peptidase S1A.
 DR InterPro: IPR009003; Pept_Ser_Cys.
 DR Pfam: PF00089; Trypsin; 1.
 DR PRINTS: PR00722; CHYMOTRYPSIN.
 DR PRODOM: PD001827; Histone H4; 1.
 DR PROSITE: PS00134; TRYPSIN_HIS; UNKNOWN 1.
 KW Hydrolase: Hypothetical protein; Protease; Serine protease.
 SQ SEQUENCE 383 AA; 41159 MW; 4AB12CC7B66CDFC8 CRC64;

Query Match 89.3%; Score 1903; DB 2; Length 383;
 Best Local Similarity 91.4%; Pred. No. 1.3e-152;
 Matches 350; Conservative 11; Mismatches 22; Indels 0; Gaps 0;

QY 1 MAGTGLLLFLLFLLCAVGVSVSPKPKTWPAYRLPVVLPOSTLNLAKEPFGAEAKLE 60
 DB 1 MAGTGLLLFLLFLLVLLCVFMQVSPVNPWKPTWPAYRLPVVLPOSTLNLAKEPFGAEAKLE 60

QY 61 VSSSCGPOCHKGTPLPTYEAKQVLSYETLYANGSRRTQVGIYILSSSGDGAQHRS DGS 120
 DB 61 VSSSCGPOCHKGTPLPTYEAKQVLSYETLYANGSRRTQVGIYILSSSGDGAQHRS DGS 120

QY 121 SGKSRKRQIYGVDSRPSIFGKDFLLNYPSTSVKLTGCTGLVAEKHVLTAACHIDG 180
 DB 121 AGKSRKRQIYGVDSRPSIFGKDFLLNYPSTSVKLTGCTGLVAEKHVLTAACHIDG 180

QY 181 KTVYVGTQKLVGFLPKPKFGKGRGANDSTAMPQKFWIRVKTHTVDPKGIKGNAND 240
 DB 181 KTVYVGTQKLVGFLPKPKFGKGRGANDSTAMPQKFWIRVKTHTVDPKGIKGNAND 240

QY 241 IGMDDYDYLLEKPKPKMKIGVSPPAKLPGRTHFSGYNDNRPNGLVYRFPDVKDE 300
 DB 241 IGMDDYDYLLEKPKPKMKIGVSPPAKLPGRTHFSGYNDNRPNGLVYRFPDVKDE 300

QY 301 TYDLLYQCCDAQPCAGSGGVYVVRMKRQKQKWKRIIGIFSGHQWDMNGSPQDFNVAVR 360
 DB 301 TYDLLYQCCDAQPCAGSGGVYVVRMKRQKQKWKRIIGIFSGHQWDMNGSPQDFNVAVR 360

QY 361 ITPKVAQICWIKGNLYDCRG 383
 DB 361 ITPKVAQICWIKGNLYDCRG 383

RESULT 3

PS23_MOUSE STANDARD; PRT; 382 AA.
 AC Q9D6X6; Q8VEG1;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 25-OCT-2004 (Rel. 45, Last annotation update)
 DE Serine protease 23 precursor (EC 3.4.21.-).
 GN Name=Prse23;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OC NCBI_TaxID=10090;
 RN [1]
 RN SEQUENCE FROM N.A.
 RP STRAIN=C57BL/6J; TISSUE=Tongue;
 RC MDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
 RX Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
 RA Nikaide I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
 RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,
 RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
 RA Schriml L.M., Kanapin A., Mateuda H., Batalov S., Beisel K.W.,
 RA Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,
 RA Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,
 RA Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
 RA Grimmond S., Guetincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
 RA Kanai A., Kawai H., Kawasawa Y., Kedzierzki R.M., King B.L.,
 RA Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
 RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
 RA Nagashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,
 RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,

RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
 RA Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K.,
 RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
 RA Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,
 RA Wilming L.G., Wyndham-Boris A., Yanagisawa M., Yang I., Yang L.,
 RA Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
 RA Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
 RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
 RA Hara A., Haeishizume W., Imotani K., Ishii Y., Iton M., Kagawa I.,
 RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
 RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
 RA Birney E., Hayashizaki Y.;
 RT "Analysis of the mouse transcriptome based on functional annotation of
 RT 60,770 full-length cDNAs.";
 RL Nature 420:563-573 (2002).
 RP SEQUENCE FROM N.A.
 RP TISSUE=Breast tumor;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.F., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Uesdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalek U., Smalish D.E.,
 RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 CC -1- SUBCELLULAR LOCATION: Secreted (Potential).
 CC -1- SIMILARITY: Belongs to the peptidase S1 family.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL: AK009847; BAB26541.1; -;
 DR EMBL: AK078518; BAC37319.1; -;
 DR EMBL: BC018517; AAB18517.1; -;
 DR HSP: P00746; IDSU.
 DR MEROPS: S01.309; -;
 DR MGI: 1923703; 2310046G15Rik.
 DR InterPro: IPR009003; Pept_Ser_Cys.
 DR InterPro: IPR001254; Peptidase_S1.
 DR InterPro: IPR001314; Peptidase_S1A.
 DR Pfam: PF00089; Trypsin; 1.
 DR PRINTS: PR00722; CHYMOTRYPSIN.
 DR SMART: SM00020; TRYP_SPC; 1.
 DR PROSITE: PS00240; TRYPSIN_DOM; FALSE_NEG.
 DR PROSITE: PS00134; TRYPSIN_HIS; 1.
 DR PROSITE: PS00135; TRYPSIN_SER; FALSE_NEG.
 KW Hydrolase; Serine protease; Signal.
 FT SIGNAL 1 22 Potential.
 FT CHAIN 23 382 Serine protease 23.
 FT ACT_SITE 174 174 Charge relay system (By similarity).
 FT ACT_SITE 239 239 Charge relay system (By similarity).
 FT ACT_SITE 315 315 Charge relay system (By similarity).
 FT DISULFID 159 175 By similarity.
 FT CARBOHYD 92 92 N-linked (GlcNAc...) (Potential).

FT CARBOHYD 206 206 N-linked (GlcNAc...) (Potential).
FT CONFLICT 260 260 M -> I (in Ref. 1; BAB26541).
SQ SEQUENCE 382 AA; 43071 MW; 6F09A5C80A5B2306 CRC64;

Query Match 88.6%; Score 1888.5; DB 1; Length 382;
Best Local Similarity 90.9%; Pred. No. 2.1e-151;
Matches 348; Conservative 14; Mismatches 20; Indels 1; Gaps 1;

QY 1 MAGIPGLFLFLFLLCAVGVSPYSAPWKPWPAYRLPVVLPQSTLNLAQKADFGABAKLE 60
DB 1 MAGIPG-LFILLVLLCVFMQVSPYTPWKPWPAYRLPVVLPQSTLNLAQKADFGABAKLE 59

QY 61 VSSCGPQCHKGTPLTPTYEAAKQYLSYETLYANGSRTETQVGIYILSSGGAQHRDSSG 120
DB VSSCGPQCHKGTPLTPTYEAAKQYLSYETLYANGSRTETQVGIYILSSGGAQHRDSSG 119

QY 121 SGKSRKRQIYGYDSRPSIFGKDFLLNYPFSTSVKLSGCTGTLVAEKHVLTAACHIDG 180
DB TGRSRKRQIYGYDSRPSIFGKDFLLNYPFSTSVKLSGCTGTLVAEKHVLTAACHIDG 179

QY 181 KTYVKGTKLVRGVFLKPKFKDGGGRANDTSAMPQMKFQWIRVKTHTVHPKGIKNAND 240
DB KTYVKGTKLVRGVFLKPKFKDGGGRANDTSAMPQMKFQWIRVKTHTVHPKGIKNAND 239

QY 241 IGMDDYALFLLKPKHFKPMKIGVSPPAKQLPGGRHFGSYNDNDRPNLVYRFDVKDE 300
DB IGMDDYALFLLKPKHFKPMKIGVSPPAKQLPGGRHFGSYNDNDRPNLVYRFDVKDE 299

QY 301 TYDLLYQCCDAQPGAGSGGVYVWMKRCQKQKWKRIIGIFPSGHWDMNGSPQDFNVAVR 360
DB TYDLLYQCCDAQPGAGSGGVYVWMKRCQKQKWKRIIGIFPSGHWDMNGSPQDFNVAVR 359

QY 361 ITELKVAQICWYIKGNLYDCREG 383
DB ITELKVAQICWYIKGNLYDCREG 382

RESULT 4
Q8BZS4 PRELIMINARY; PRT; 382 AA.
ID Q8BZS4
AC Q8BZS4
DT 01-MAR-2003 (TEMBLrel. 23, Created)
DT 01-MAR-2003 (TEMBLrel. 23, Last sequence update)
DE Mus musculus adult male cecum cDNA, RIKEN full-length enriched
DE library, clone:9130215B18 product:SERINE PROTEASE (HYPOTHETICAL 43.0
DE kDa PROTEIN) (PROTEASE, SERINE, 23) homolog.
OS Mus musculus (Mouse)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Cecum;
RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA Carninci P., Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning."
RL Meth. Enzymol. 303:19-44(1999).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Cecum;
RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA RIKEN FANTOM Consortium;
RT "Functional annotation of a full-length mouse cDNA collection."
RL Nature 409:685-690(2001).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Cecum;
RA The FANTOM Consortium;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs."
RL Nature 420:563-573(2002).

RNA SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Cecum;
RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
RT prepare full-length cDNA libraries for rapid discovery of new genes."
RL Genome Res. 10:1617-1630(2000).
RN [5]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Cecum;
RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA Konno H., Akiyama J., Nishi K., Kitsuai T., Tashiro H., Itoh M.,
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA Fujisawa S., Inoue K., Togawa Y., Izawa K., Ohara E., Watahiki M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system-384-format
RT sequencing pipeline with 384 multicapillary sequencer."
RL Genome Res. 10:1757-1771(2000).
RN [6]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Cecum;
RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
RA Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
RA Horii F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Koyama S.,
RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
RA Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
RA Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: Belongs to peptidase family S1.
DR EMBL; AK033671; BAC28420.1; -
DR GO; GO:0004263; F:chymotrypsin activity; IEA.
DR GO; GO:0008233; F:peptidase activity; IEA.
DR GO; GO:0004295; F:trypsin activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR001254; Peptidase S1.
DR InterPro; IPR001314; Peptidase S1A.
DR InterPro; IPR009003; Pept Ser_Cys.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR SMART; SM00020; Tryp_SPC; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.
KW Hydrolase; Hypothetical protein; Protease; Serine protease.
SQ SEQUENCE 382 AA; 43147 MW; 556789818E12A081 CRC64;

Query Match 88.3%; Score 1882.5; DB 2; Length 382;
Best Local Similarity 90.6%; Pred. No. 6.8e-151;
Matches 347; Conservative 14; Mismatches 21; Indels 1; Gaps 1;

QY 1 MAGIPGLFLFLFLLCAVGVSPYSAPWKPWPAYRLPVVLPQSTLNLAQKADFGABAKLE 60
DB 1 MAGIPG-LFILLVLLCVFMQVSPYTPWKPWPAYRLPVVLPQSTLNLAQKADFGABAKLE 59

QY 61 VSSCGPQCHKGTPLTPTYEAAKQYLSYETLYANGSRTETQVGIYILSSGGAQHRDSSG 120
DB VSSCGPQCHKGTPLTPTYEAAKQYLSYETLYANGSRTETQVGIYILSSGGAQHRDSEA 119

QY 121 SGKSRKRQIYGYDSRPSIFGKDFLLNYPFSTSVKLSGCTGTLVAEKHVLTAACHIDG 180
DB TGRSRKRQIYGYDSRPSIFGKDFLLNYPFSTSVKLSGCTGTLVAEKHVLTAACHIDG 179

QY 181 KTYVKGTKLVRGVFLKPKFKDGGGRANDTSAMPQMKFQWIRVKTHTVHPKGIKNAND 240
DB KTYVKGTKLVRGVFLKPKFKDGGGRANDTSAMPQMKFQWIRVKTHTVHPKGIKNAND 239

241 IGMDDYDYLLEKPKHKKFKMKGVSPPAKQLPGGRHFGSYDNDPGLNLYVRFCDVKDE 300
 240 IGMDDYDYLLEKPKHKKFKMKGVSPPAKQLPGGRHFGSYDNDPGLNLYVRFCDVKDE 299
 301 TYDLYLQQCDAQPGASGSGVYVVRWKRQKQKWKRIIGIPSGHQMVGMSQDFNVAVR 360
 300 TYDLYLQQCDAQPGASGSGVYVVRWKRQKQKWKRIIGIPSGHQMVGMSQDFNVAVR 359
 361 ITPKYAQICWIKGNLYDCREG 383
 360 ITPKYAQICWIKGNLYDCREG 382

RESULT 5
 Q9BQ6 PRELIMINARY; PRT; 413 AA.

AC Q9BQ6; (Tremblrel. 17, Created)
 DT 01-JUN-2001 (Tremblrel. 17, Last sequence update)
 DT 01-JUN-2001 (Tremblrel. 17, Last sequence update)
 DT 01-MAR-2004 (Tremblrel. 26, Last annotation update)
 DE D1223E3.1 (Putative secreted protein ZS1G13).
 GN Names=dJ223E3.1;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Dunn M.;
 RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
 RC -1- SIMILARITY: Belongs to peptidase family S1.
 DR EMBL; AL121939; CAC35071.1; -;
 DR MEROPS; S01.994; -; PRSS35.
 DR Genew; HGNC:21387; PRSS35.
 DR GO; GO:0004263; F:chymotrypsin activity; IEA.
 DR GO; GO:0008233; F:peptidase activity; IEA.
 DR GO; GO:0004295; F:trypsin activity; IEA.
 DR GO; GO:000508; P:proteolysis and peptidolysis; IEA.
 DR InterPro; IPR01254; Peptidase S1.
 DR InterPro; IPR01314; Peptidase S1A.
 DR InterPro; IPR009003; Pept Ser_Cys.
 DR Pfam; PF00089; Trypsin; 1.
 DR PRINTS; PR00722; CHYMOTRYPSIN.
 DR SMART; SM00020; Tryp_SPC; 1.
 DR PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.
 KW Hydrolase; Protease; Serine protease.
 SQ SEQUENCE 413 AA; 47098 MW; 818D9C951BD2D6C1 CRC64;

Query Match 48.9%; Score 1042; DB 2; Length 413;
 Best Local Similarity 47.8%; Pred. No. 1.1e-79;
 Matches 200; Conservative 68; Mismatches 100; Indels 50; Gaps 7;

QY 7 LAFLLFLLCAVG--QVSPVSAWKPTWPAAYRLPVVLPOSTLNLAKPDFGAELKLVSSS 64
 DB 5 LLWLIF--TPQWTLDSGEMEDFWHLKRVPRIVSERTFHLTSPAEADAKMNVV 61
 QY 65 CGPQCHGTPLPYERAKQVLSYETLYANGSRFTQVGI--YTLSSGGCAQHRDSSGS 122
 DB 62 CGIECQKELTPSLSELYSYETVFENGTRTLTRVKQDLVLEPT-----QNITTKG 115
 QY 123 KS--RRKQYGVDSRSIFGKDFLLNYPSTSVKLTGCTGLVAEKLVLTAHCIDGK 181
 DB 116 VSVRRKQVGTDSRSIFLIDKRLTFNPFSTAVKLSTGCGILISQHVLTAAHCVDHGK 175
 QY 182 TVYKGTQKRLVGLPKFKDQGR-----GANDSTSAHPQMK----- 218
 DB 176 DYVKGSKLVGLLKNKSGGKRGSKRSREASGGQDRETRHLERAKGRRRK 235
 QY 219 -----FQWIRVTRHPKGIWKNANDIGMDYDYLLEKPKHKKFKMKGIV 265
 DB 236 SGRGRIAEGRPSFQWIRVTRHPKGIWKNANDIGMDYDYLLEKPKHKKFKMKGIV 295
 QY 266 SPPAKQLPGGRHFGSYDNDPGLNLYVRFCDVKDEYDLYLQQCDAQPGASGSGVYVVRW 325

Db 296 SPTIKKMPGMIHFSGFNDRADQLVYRFSVDSNDLLQYCDAESGSGTSGVYLRK 355
 QY 326 KRQOQKWKRIIGIPSGHQMVGMSQDFNVAVRITPLKYAQICWIKGNLYDCREG 383
 Db 356 DPDKKWKRIIAVYSGHQMVGVDVHGQKDYNAVAVRITPLKYAQICLWIHGNDANCAYG 413

RESULT 6
 Q8N320 PRELIMINARY; PRT; 413 AA.

AC Q8N320;
 DT 01-OCT-2002 (Tremblrel. 22, Created)
 DT 01-OCT-2002 (Tremblrel. 22, Last sequence update)
 DT 25-OCT-2004 (Tremblrel. 28, Last annotation update)
 DE Hypothetical protein PRSS35 (ENML522).
 GN Name=PRSS35; ORFNames=UNQ522;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA TISSUE=Brain;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
 RA Jones S.J., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Strausberg R.;
 RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=2287296; PubMed=12975309; DOI=10.1101/gr.1293003;
 RA Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D., Brush J.,
 RA Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,
 RA Eaton D., Foster J., Grimaldi C., Gu Q., Hass P.E., Heldens S.,
 RA Huang A., Kim H.S., Klinkowski L., Jin Y., Johnson S., Lee J.,
 RA Lewis L., Liao D., Mark M., Robbie E., Sanchez C., Schoenfeld J.,
 RA Seshagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A.,
 RA Vandlen R., Watanabe C., Wieand D., Woods K., Xie M.H., Yansura D.,
 RA Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I.,
 RA Godowski P.;
 RT "The secreted protein discovery initiative (SPDI), a large-scale
 effort to identify novel human secreted and transmembrane proteins: a
 bioinformatics assessment.";
 RL Genome Res. 13:2265-2270(2003).
 CC -1- SIMILARITY: Belongs to peptidase family S1.
 DR EMBL; BC037170; AAH37170.1; -;
 DR EMBL; AY358661; AAQ89024.1; -;
 DR GO; GO:0004263; F:chymotrypsin activity; IEA.
 DR GO; GO:0008233; F:peptidase activity; IEA.
 DR GO; GO:0004295; F:trypsin activity; IEA.
 DR GO; GO:000508; P:proteolysis and peptidolysis; IEA.

RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Belongs to peptidase family S1.

DR EMBL; AK031411; BAC27392.1; -;
DR EMBL; BC075675; AAH75675.1; -;
DR MGD; MGI:2444800; Prs935.
DR GO; GO:0005615; C:extracellular space; TAS.
DR InterPro; IPR001254; Peptidase_S1.
DR InterPro; IPR001314; Peptidase_S1A.
DR InterPro; IPR009003; Pept_Ser_Cys.
DR Pfam; PF00089; Trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR SMART; SM00020; Tryp_SPC; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.
DR Hydrolase; Protease; Serine protease.
KW SEQUENCE 409 AA; 45787 MW; 5E2D24A908E7EF5 CRC64;

Query Match 47.7%; Score 1016.5; DB 2; Length 409;
Best Local Similarity 49.4%; Pred. No. 1.6e-77;
Matches 193; Conservative 68; Mismatches 83; Indels 47; Gaps 5;

QY 31 TWPAYRLPVLPVLPSTLNLAKEPDAEAKLEVSQCGPQCHGKGTPLTYEEAKQYLSYETL 90
DB 28 TWHLRIPOVQVSENTIHLASPTFOAGVVKATVCGIECOELPAPSLQLESLSYETI 87
QY 91 YANGSRTEQVGVIL-----SSSGDGAQHRDSSGSKRRKRYGYDSRFSIFGKDF 144
DB 88 FENGTHLTRVQGLVLETRNSVKGAH-----PRRRQVYGTDSRFSILDKRF 138
QY 145 LLNYPFSTSVKLTGCTGTVAEKHVLTAACHDGTYYKQKLRVGLPKPKFDG-- 202
DB 139 ATNFPNTAVKLTGCGTLVSPNHVLTAAHCVDHGDYVYKSGKLRVGLVKNRNGGRK 198
QY 203 -GRGA-----NDSTSAMPEQM-----KFWIRVTRVTHVPKG 232
DB 199 KRGSKRSRREARSAGOSQAHLESTTQREGKSRGRPRVTQGRSPQWTRVXSTHPKG 258
QY 233 WIKGNANDIGMDYDYLLELKKPKRKFMIKIGVSPPAKQLPGGRIFHSGYDNDPRGNLVY 292
DB 259 WVRGEGGLALDYDYLLELKRHAHQHMLGVSPTITKLPGGRIFHSGFDNDRDQLVY 318
QY 293 RFDVDRDTEYDLYQQCDAQPGASGVYVVMKQQQKWERKIIIFSGHGWDMNGSP 352
DB 319 RFCSVSEESNDLLYQYCDAEAGSTGSGIYLRLEKPGQKNKRIKIVAVYSGHWDVHGQ 378
QY 353 QDNVAVRITPLKYAQICWIKGNYLDCREG 383
DB 379 KQYNAVVRITPLKYAQICLWINGNAANCAYG 409

RESULT 8

Q6GML6
ID Q6GML6 PRELIMINARY; PRT; 418 AA.
AC Q6GML6;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Zgc:91804.
GN ORFNames=zgc:91804;
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Whole;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.O., Hulyk S.W.,
RA Villalon D.K., Muzny K.C., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smallos D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Whole;
RA Strausberg R.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC074028; AAH74028.1; -;
DR ZFIN; ZDB-GENE-040704-55; zgc:91804.
DR GO; GO:0008233; F:peptidase activity; IEA.
DR GO; GO:0004295; F:trypsin activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR001254; Peptidase_S1.
DR InterPro; IPR009003; Pept_Ser_Cys.
DR Pfam; PF00089; Trypsin; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.
KW Hydrolase; Protease; Serine protease.
SQ SEQUENCE 418 AA; 47270 MW; AF53345CEB94F720 CRC64;

Query Match 47.6%; Score 1014.5; DB 2; Length 418;
Best Local Similarity 46.6%; Pred. No. 2.4e-77;
Matches 196; Conservative 64; Mismatches 118; Indels 43; Gaps 2;

QY 1 MAGIPCLLFLFLCAVGVSPYSAPWKPPTPAVLPVLPSTLNLAKEPDAEAKLE 60
DB 1 MGPVPLTLLLSALAVLSTTVDPTGDTYTPQKIPLVQEKQTVHLSSEFLAKPND 60
QY 61 VSSCGPQCHGKGTPLTYEEAKQYLSYETLYANGSRTEQVGIYILSSGCGAQHRDSSG 120
DB 61 LHGICGIECQRLPEPSLDLEQLLSYETMYDNGTRTLTTVTQDLNVSNDWT---GAS 116
QY 121 SKSRKRIYGYDSRFSIFGKDFLLNYPFSTSVKLTGCTGTVAEKHVLTAACHDHC 180
DB 117 QLHTRHREYVGTDRFTITDKOYSMKYPFSTSVKLTGCGVLVSPKHLVTAACHHNG 176
QY 181 KTYVKGTKLRVGLKP-----KFKD 201
DB 177 TYLDGVQLKLVGLKRSRRKRGKRGKRGKRGKRGKRGKRGKRGKRGKRGKRGK 236
QY 202 GGRGANDSTAMPQMKFQWIRVTRVTHVPKGIKGNANDIGMDYDYLLELKKPKRKF 261
DB 237 KGRNRSRSTDSQSPFRWTRVKQVQKGFISENVLADYDVALELKRQAKTKFM 296
QY 262 KIGVSPPAKQLPGGRIFHSGYDNDPRGNLVYFCDVKDTEYDLYQQCDAQPGASGVY 321
DB 297 DLGVIPSVKLLPAGRIHFSFGDDPRGNLVYFCSVSEESNDLLYQYCDAKPGSSGVY 356
QY 322 VVMKRGQQKWERKIIIFSGHGWDMNGSPDENVAVRITPLKYAQICWIKGNVLDCH 381
DB 357 IRLKPGKKKKRKLIGVFGHGWVNGQQQDYNVAVRITPLKYAQICRWVHGDSSQCR 416
QY 382 E 382
DB 417 D 417

RESULT 9

Q8COL5
ID Q8COL5 PRELIMINARY; PRT; 409 AA.
AC Q8COL5;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)

RN [3] SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Testis;
 RA The FANTOM Consortium,
 RA the RIKEN Genome Exploration Research Group Phase I & II Team;
 RT "Analysis of the mouse transcriptome based on functional annotation of
 RT 60,770 full-length cDNAs.";
 RL Nature 420:563-573(2002).
 RN [4]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Testis;
 RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
 RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
 RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
 RT "Normalization and subtraction of cap-trapper-selected cDNAs to
 RT prepare full-length cDNA libraries for rapid discovery of new genes.";
 RL Genome Res. 10:1617-1630(2000).
 RN [5]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Testis;
 RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
 RA Shibata K., Itoh M., Aizawa K., Nagao S., Sasaki N., Carninci P.,
 RA Konno H., Akiyama J., Nishi K., Kitsuai T., Tashiro H., Itoh M.,
 RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
 RA Yamamoto R., Matsuoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
 RA Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Watabiki M.,
 RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
 RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
 RT "RIKEN integrated sequence analysis (RISA) system-384-format
 RT sequencing pipeline with 384 multicapillary sequencer.";
 RL Genome Res. 10:1757-1771(2000).
 RN [6]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Testis;
 RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
 RA Fukuda S., Furuno M., Hanganaki T., Hara A., Hashizume W.,
 RA Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
 RA Hori F., Imotani K., Ishii Y., Itoh M., Kegawa T., Kasukawa T.,
 RA Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,
 RA Kurihara K., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
 RA Nishi K., Nomura K., Numazaki R., Ono M., Ohsato N., Okazaki Y.,
 RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
 RA Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
 RA Tagawa A., Takahashi F., Takaku-Akashira S., Takeda Y., Tanaka I.,
 RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AK031644; BAC27491.1; -;
 DR MGD; MGI:2444800; P8835.
 DR GO; GO:0005615; C:extracellular space; TAS.
 DR InterPro; IPR001254; Peptidase_S1.
 DR InterPro; IPR009003; Pept_Ser_Cys.
 DR Pfam; PF00089; Trypsin; 1.
 DR SMART; SM00020; Tryp_Spc; 1.
 DR Hydrolase; Protease; Serine protease.
 KW SEQUENCE 409 AA; 45736 MW; E9C9B9156800719C CRC64;
 SQ
 Query Match 47.2%; Score 1005.5; DB 2; Length 409;
 Best Local Similarity 48.8%; Pred. No. 1.4e-76;
 Matches 191; Conservative 70; Mismatches 83; Indels 47; Gaps 5;
 QY 31 TWPAYRLPVLPQSTLNLAQDFGAELVSSGCGQCHGTPLPYEAKQYLSYETL 90
 DB 28 TWLSRLPQVSVTHIHLASPTQADAGVVKATVCGIECQEEPLPAPLSQLESLSYETI 87
 QY 91 YANGSRTEQVGIYL-----SSSGDAQHRDSGSGSKRRKQIYGYDSRFSIFKQDF 144
 DB 88 FENGTRTLTRVKQGLVLETRNSSVKGAH-----PRRRQVGTDSRFSILDKRF 138
 QY 145 LLNYPFSTSVKLSGCTGTLVAEKHVLTAACHIDGKTYVKGTKLRVGLKPKFKDG-- 202
 DB 139 ATNFPFNTAVKLSGCTGLVSPNHLTAANCVDHGDYKVGSKLAVGLKVRNKGGRK 198
 QY 203 -GRGA-----NDSTSAMPEQM-----KQWIRVRKTRTHVPKG 232

Db 199 KRGRSKSRREASAGSOAHLESITQRPKSKRRGPRVTQGRPPSFQWTRVKSHTIPKG 258
 QY 233 WIKGNANDIGMDYDVALLELKKPKFKMIGVSPPAKQIPGGRHIFSGYDNDPRGNLVY 292
 Db 259 WVRGEGGLADYDVALLELKKRAHKQOHMELGVSPTITKLPGQIHFSGFNDRDEQLVY 318
 QY 293 RFDVNDYDLYOOCDAQPGASGGVYVMKROOKWERTKIIGFSGHGWDMNGSP 352
 Db 319 RRCVSEESNDLLYQYCDAAEGSTGSGIYLRLEKPGQKNWKRKIVAVYSGHWDVDRHGQ 378
 QY 353 QDNVAVRITPLKYAQICVYKGNLYDCREG 383
 Db 379 KDYNVAVRITPLKYAQICLWIHGNAACVAG 409
 RESULT 11
 ID GSEP_BACLI STANDARD; PRT; 316 AA.
 AC P80057;
 DT 01-MAY-1992 (Rel. 22, Created)
 DT 01-OCT-1993 (Rel. 27, Last sequence update)
 DT 25-OCT-2004 (Rel. 45, Last annotation update)
 DE Glutamyl endopeptidase precursor (SC 3.4.21.19) (Glutamate specific
 DE endopeptidase) (GSE).
 GN Name:blase;
 OS Bacillus licheniformis.
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
 OC NCBI_TaxID=1402;
 RN [1]
 RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
 RC STRAIN=ATCC 14580;
 RX MEDLINE=93054737; PubMed=1429718;
 RA Kakudo S., Kikuchi N., Kitadokoro K., Fujiwara T., Nakamura E.,
 RA Okamoto H., Shin M., Tamaki M., Teraoka H., Tazuki H., Yoshida N.;
 RT "Purification, characterization, cloning, and expression of a glutamic
 RT acid-specific protease from Bacillus licheniformis ATCC 14580.";
 RL J. Biol. Chem. 267:23782-23788(1992).
 RN [2]
 RP SEQUENCE OF 95-316.
 RX MEDLINE=92155199; PubMed=1346764;
 RA Svendsen I., Bredam K.;
 RT "Isolation and amino acid sequence of a glutamic acid specific
 RT endopeptidase from Bacillus licheniformis.";
 RL Eur. J. Biochem. 204:165-171(1992).
 CC -1- FUNCTION: Specific for hydrolysis of peptide bonds on the carboxyl
 CC side of acidic amino acid residues, with a strong preference for
 CC Glu.
 CC -1- CATALYTIC ACTIVITY: Preferential cleavage: Asp-|-Xaa, Glu-|-Xaa.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- SIMILARITY: Belongs to the peptidase S1B family.
 CC
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
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 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC
 CC EMBL; D10060; BAA00949.1; -;
 DR PIR; A45134; A45134.
 DR MEROPS; S01.271; -;
 DR InterPro; IPR000126; Pept_S1B_AS.
 DR InterPro; IPR009003; Pept_Ser_Cys.
 DR InterPro; IPR001254; Peptidase_S1.
 DR InterPro; IPR008256; Peptidase_S1B.
 DR Pfam; PF00089; Trypsin; 1.
 DR PRINTS; PR00839; V8PROTEASE.
 DR SMART; SM00020; Tryp_Spc; 1.
 DR PROSITE; PS00672; V8_HIS; 1.
 DR PROSITE; PS00673; V8_SER; 1.
 KW Direct protein sequencing; Hydrolase; Serine protease; Signal.

Search completed: July 1, 2005, 21:08:12
Job time : 94.7095 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: July 1, 2005, 20:52:53 ; Search time 98.1294 Seconds
(without alignment)
1509.530 Million cell updates/sec

Title: US-09-658-677-18

Perfect score: 2080

Sequence: 1 MAGIPGLFLFLFLCAVGQ.....LKVAICYWIKGNVLDREG 383

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: Geneseqp16Dec04:*

2: Geneseqp1980s:*

3: Geneseqp1980s:*

4: Geneseqp2000s:*

5: Geneseqp2001s:*

6: Geneseqp2002s:*

7: Geneseqp2003as:*

8: Geneseqp2003bs:*

9: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB ID	Description
1	2080	100.0	383	2	AAY08660 WO9927094
2	2080	100.0	383	2	AAY08657 Human tra
3	2080	100.0	383	2	AAY13390 Amino aci
4	2080	100.0	383	3	AAY88277 Human TAN
5	2080	100.0	383	3	AAY87270 Human sig
6	2080	100.0	383	3	AAY53627 A bone ma
7	2080	100.0	383	3	AAB25618 Protein e
8	2080	100.0	383	3	AAB25592 Protein e
9	2080	100.0	383	3	ADC78573 Human PRO
10	2080	100.0	383	4	AAB80258 Human PRO
11	2080	100.0	383	4	AAB48974 Human Zsi
12	2080	100.0	383	4	AAB29048 Human PRO
13	2080	100.0	383	6	ABU58424 Human PRO
14	2080	100.0	383	6	ABU71636 Human PRO
15	2080	100.0	383	6	ABU87972 Novel hum
16	2080	100.0	383	6	ABU84287 Human sec
17	2080	100.0	383	6	ABR66161 Human sec
18	2080	100.0	383	6	ABR65551 Human sec
19	2080	100.0	383	6	ABU99491 Human sec
20	2080	100.0	383	6	ABU82730 Human PRO
21	2080	100.0	383	6	ABU89851 Novel hum
22	2080	100.0	383	6	ABU71491 Human PRO
23	2080	100.0	383	6	ABR68100 Human sec
24	2080	100.0	383	6	ABU96153 Novel hum
25	2080	100.0	383	6	ABU92584 Human sec

26	2080	100.0	383	6	ABO08661	Abu08661 Human sec
27	2080	100.0	383	6	ABO02713	Abu02713 Human sec
28	2080	100.0	383	6	ABR74867	Abu74867 Human sec
29	2080	100.0	383	6	ABR94629	Abu94629 Human sec
30	2080	100.0	383	6	ABU85602	Abu85602 Human PRO
31	2080	100.0	383	6	ABU98762	Abu98762 Novel hum
32	2080	100.0	383	6	ABU97977	Abu97977 Novel hum
33	2080	100.0	383	6	ABU91683	Abu91683 Novel hum
34	2080	100.0	383	6	ABU71937	Abu71937 Human sec
35	2080	100.0	383	6	ABU89376	Abu89376 Human PRO
36	2080	100.0	383	6	ABU86217	Abu86217 Human sec
37	2080	100.0	383	6	ABU67430	Abu67430 Human sec
38	2080	100.0	383	6	ABU80458	Abu80458 Human PRO
39	2080	100.0	383	6	ABO01820	Abu01820 Novel hum
40	2080	100.0	383	6	ABR99376	Abu99376 Human sec
41	2080	100.0	383	6	ABR98766	Abu98766 Human sec
42	2080	100.0	383	6	ABO16289	Abu16289 Human sec
43	2080	100.0	383	6	ABR92189	Abu92189 Human sec
44	2080	100.0	383	6	ABO18830	Abu18830 Human sec
45	2080	100.0	383	6	ABR78251	Abu78251 Human sec

ALIGNMENTS

RESULT 1

AAY08660
ID AAY08660 standard; protein; 383 AA.

XX AC AAY08660;

XX AC AAY08660;

DT 09-AUG-1999 (first entry)

XX WO9927094 Seq ID 12.

XX WO9927094 Seq ID 12.

KW Transmembrane domain; human; nutrition; cytokine; cell differentiation;

KW immune stimulation; immune suppression; haematopoiesis; activin;

KW regulatory tissue growth; inhibitor; chemostatic; chemokinetic;

KW haemostatic; thrombolytic; tumour inhibitor; anti-inflammatory;

KW gene therapy; screening.

XX Homo sapiens.

XX WO9927094-A2.

XX 03-JUN-1999.

XX 20-NOV-1998; 98WO-JP005238.

XX 25-NOV-1997; 97JP-00323129.

XX (SAGA) SAGAMI CHEM RES CENT.

PA (PROT-) PROTEGENE INC.

XX Kato S, Kimura T, Sekine S;

PI WPI; 1999-357835/30.

XX Novel proteins containing transmembrane domains, useful as anti-

XX inflammatories, immune stimulators/suppressors and tissue growth

XX compounds.

XX Disclosure; Page 87-89; 89pp; English.

XX This invention describes novel human transmembrane containing proteins

XX and their encoding nucleic acids. Although no specific use is given for

XX the proteins, they may have a range of activities selected from

XX nutritional uses, cytokine and cell differentiation, immune

XX stimulation/suppression, haematopoiesis regulatory, tissue growth,

XX activin/inhibin, chemostatic/chemokinetic, haemostatic/thrombolytic,

XX receptor/ligand, tumour inhibitor, anti-inflammatory and other undefined

XX activities. The cDNAs can be utilized as probes for gene diagnosis and as

XX gene sources for gene therapy. The cDNAs can also be used for large scale

CC expression of proteins. The transformed cells can be used for detection
CC of the corresponding ligands and for screening of novel low-molecular
CC pharmaceuticals
XX
SQ Sequence 383 AA;

Query Match 100.0%; Score 2080; DB 2; Length 383;
Best Local Similarity 100.0%; Pred. No. 1.8e-145;
Matches 383; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAGIPGLLFLFLCAVGVSPYSAPWKPTWPAYRLPVVLPQSTLNLAKEPFGAEAKLE 60
DB 1 MAGIPGLLFLFLCAVGVSPYSAPWKPTWPAYRLPVVLPQSTLNLAKEPFGAEAKLE 60

QY 61 VSSSCGQCHKGTPPTYEAKQYLSYETLYANGSRSTETQVGIYILSSSGDGAQHRDGS 120
DB 61 VSSSCGQCHKGTPPTYEAKQYLSYETLYANGSRSTETQVGIYILSSSGDGAQHRDGS 120

QY 121 SGKRRKRQIYGDSRFSIFGKDFLLNYPFSTSVKLSGTGCTGLVAEKHVLTAACHIDG 180
DB 121 SGKRRKRQIYGDSRFSIFGKDFLLNYPFSTSVKLSGTGCTGLVAEKHVLTAACHIDG 180

QY 181 KTYVKGTKLRVGLKPKFKDGGRGANDSTSAMPEQMKFQWIRVKTHTVPKGIKGNAND 240
DB 181 KTYVKGTKLRVGLKPKFKDGGRGANDSTSAMPEQMKFQWIRVKTHTVPKGIKGNAND 240

QY 241 IGMDDYALLELKKPKHKFKMKIGVSPPAKQLPGRIHFSGYDNDPGLNLYRFGCDVKDE 300
DB 241 IGMDDYALLELKKPKHKFKMKIGVSPPAKQLPGRIHFSGYDNDPGLNLYRFGCDVKDE 300

QY 301 TYDLLYQQCDAQPGASGSGVYVRMWKQQKWERKIIIGIFSGHWDMDNGSPQDFNVAVR 360
DB 301 TYDLLYQQCDAQPGASGSGVYVRMWKQQKWERKIIIGIFSGHWDMDNGSPQDFNVAVR 360

QY 361 ITPLKYAQCICWIKGNLYDCREG 383
DB 361 ITPLKYAQCICWIKGNLYDCREG 383

RESULT 2
AAY08657
ID AAY08657 standard; protein; 383 AA.
AC AAY08657;
XX
XX
DT 09-AUG-1999 (first entry)
DE Human transmembrane domain containing protein from clone HP10493.
XX
KW Transmembrane domain; human; nutrition; cytokine; cell differentiation;
KW immune stimulation; immune suppression; haematopoiesis; activin;
KW regulatory tissue growth; inhibin; chemostatic; chemokinetic;
KW haemostatic; thrombolytic; tumour inhibitor; anti-inflammatory;
KW gene therapy; screening.
XX
OS Homo sapiens.
XX
XX WO9927094-A2.
XX
XX 03-JUN-1999.
XX
XX 20-NOV-1998; 98WO-JP005238.
XX
XX 25-NOV-1997; 97JP-00323129.
XX
XX (SAGA) SAGAMI CHEM RES CENT.
XX (PROT-) PROTEGENE INC.
XX
XX Kato S, Kimura T, Sekine S;
XX WPI; 1999-357835/30.
XX N-PSDB; AAX77690, AAX77691.
XX

PT Novel proteins containing transmembrane domains, useful as anti-inflammatory, immune stimulators/suppressors and tissue growth compounds.
PT
PT
XX
PS Claim 1; Page 68-69; 89pp; English.
XX
XX This invention describes novel human transmembrane containing proteins and their encoding nucleic acids. Although no specific use is given for the proteins, they may have a range of activities selected from CC nutritional uses, cytokine and cell differentiation, immune CC stimulation/suppression, haematopoiesis regulatory, tissue growth, CC activin/inhibin, chemostatic/chemokinetic, haemostatic/thrombolytic, CC receptor/ligand, tumour inhibitor, anti-inflammatory and other undefined CC activities. The cDNAs can be utilized as probes for gene diagnosis and as CC gene sources for gene therapy. The cDNAs can also be used for large scale CC expression of proteins. The transformed cells can be used for detection CC of the corresponding ligands and for screening of novel low-molecular CC pharmaceuticals
XX
SQ Sequence 383 AA;

Query Match 100.0%; Score 2080; DB 2; Length 383;
Best Local Similarity 100.0%; Pred. No. 1.8e-145;
Matches 383; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAGIPGLLFLFLCAVGVSPYSAPWKPTWPAYRLPVVLPQSTLNLAKEPFGAEAKLE 60
DB 1 MAGIPGLLFLFLCAVGVSPYSAPWKPTWPAYRLPVVLPQSTLNLAKEPFGAEAKLE 60

QY 61 VSSSCGQCHKGTPPTYEAKQYLSYETLYANGSRSTETQVGIYILSSSGDGAQHRDGS 120
DB 61 VSSSCGQCHKGTPPTYEAKQYLSYETLYANGSRSTETQVGIYILSSSGDGAQHRDGS 120

QY 121 SGKRRKRQIYGDSRFSIFGKDFLLNYPFSTSVKLSGTGCTGLVAEKHVLTAACHIDG 180
DB 121 SGKRRKRQIYGDSRFSIFGKDFLLNYPFSTSVKLSGTGCTGLVAEKHVLTAACHIDG 180

QY 181 KTYVKGTKLRVGLKPKFKDGGRGANDSTSAMPEQMKFQWIRVKTHTVPKGIKGNAND 240
DB 181 KTYVKGTKLRVGLKPKFKDGGRGANDSTSAMPEQMKFQWIRVKTHTVPKGIKGNAND 240

QY 241 IGMDDYALLELKKPKHKFKMKIGVSPPAKQLPGRIHFSGYDNDPGLNLYRFGCDVKDE 300
DB 241 IGMDDYALLELKKPKHKFKMKIGVSPPAKQLPGRIHFSGYDNDPGLNLYRFGCDVKDE 300

QY 301 TYDLLYQQCDAQPGASGSGVYVRMWKQQKWERKIIIGIFSGHWDMDNGSPQDFNVAVR 360
DB 301 TYDLLYQQCDAQPGASGSGVYVRMWKQQKWERKIIIGIFSGHWDMDNGSPQDFNVAVR 360

QY 361 ITPLKYAQCICWIKGNLYDCREG 383
DB 361 ITPLKYAQCICWIKGNLYDCREG 383

RESULT 3
AAY13390
ID AAY13390 standard; protein; 383 AA.
XX
XX AAY13390;
AC AAY13390;
XX
XX 25-JUN-1999 (first entry)
XX
XX Amino acid sequence of protein PRO307.
XX
XX Secreted protein; transmembrane protein; human; enterocolitis;
KW Zollinger-Ellison syndrome; gastrointestinal ulceration;
KW congenital microvillus atrophy; skin disease; cell growth;
KW abnormal keratinocyte differentiation; psoriasis; epithelial cancer;
KW Parkinson's disease; Alzheimer's disease; ALS; neuropathy; fibromodulin;
KW dermal scarring; Usher Syndrome; Atrophia areata; anti-thrombotic;
KW wound healing; tissue repair.
XX
XX Homo sapiens.
OS

XX PF 30-SEP-1999; 99WO-US022817.
 XX XX
 PR 30-SEP-1998; 98US-00164220.
 PR 02-OCT-1998; 98US-00164169.
 XX
 PA (MILL-) MILLENNIUM BIOTHERAPEUTICS INC.
 XX
 PI Barnes TM;
 XX
 DR WPI: 2000-293144/25
 DR N-PSDB; AAA39945, AAA39946.
 XX
 PT Isolated nucleic acids encoding TANGO polypeptides useful for preventing,
 PT diagnosing and treating diseases associated with inappropriate protein
 PT expression.
 XX
 PS Claim 9; Fig 13; 249pp; English.
 XX
 CC This invention describes novel human and murine nucleic acids encoding
 CC TANGO polypeptides (which are either wholly secreted or transmembrane
 CC proteins) which can be used for gene therapy and/or vaccination. The
 CC peptides are designated TANGO 180 to TANGO 189 and TANGO 215. The nucleic
 CC acids may be used to produce TANGO 180 to TANGO 189 and TANGO 215
 CC polypeptides according to standard recombinant DNA methodologies. They
 CC may also be used to detect and quantify the presence of TANGO nucleic
 CC acids in a sample and therefore identify or diagnose diseases associated
 CC with inappropriate TANGO expression (e.g. diseases related to over or
 CC under expression of the polypeptides or the expression of inactive
 CC polypeptides). The nucleic acids and the polypeptides they encode may be
 CC used according to standard gene therapy protocols, to treat diseases
 CC associated with inappropriate TANGO expression by supplementing a
 CC patient's own production of the polypeptide of to rectify mutations that
 CC may result in expression of an abnormally active polypeptide. The
 CC polypeptides may also be used to identify and produce agonists and
 CC antagonists of TANGO expression and activity which may be used to
 CC modulate TANGO related processes and diseases. The polypeptides are
 CC particularly useful for use as antigens for producing antibodies to TANGO
 CC proteins which may be used for inhibiting the activity of TANGO proteins.
 CC They may also be used to detect and quantify the presence of TANGO
 CC proteins in samples and therefore identify patients in whom the protein
 CC is over- or under-expressed. This sequence represents the human TANGO 186
 CC protein described in the method of the invention
 XX
 SQ Sequence 383 AA;
 Query Match 100.0%; Score 2080; DB 3; Length 383;
 Best Local Similarity 100.0%; Pred. No. 1.8e-145;
 Matches 383; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 MAGIPGLLFLFLLCVAGQVSPYSAPWKPTWPAYRLPVVLPQSTLNLAKEPFGAEAKLE 60
 Db 1 MAGIPGLLFLFLLCVAGQVSPYSAPWKPTWPAYRLPVVLPQSTLNLAKEPFGAEAKLE 60
 Qy 61 VSSCGPQCHKGTPLTYEBAKQVLSYETLYANGSRRTQVGIYILSSSGDGAQRHDSGS 120
 Db 61 VSSCGPQCHKGTPLTYEBAKQVLSYETLYANGSRRTQVGIYILSSSGDGAQRHDSGS 120
 Qy 121 SGKRRKROLYGVDRESIFGKDFLLNYPSTSVKLSGTGCTTLVAEKHVLTAACHIDHG 180
 Db 121 SGKRRKROLYGVDRESIFGKDFLLNYPSTSVKLSGTGCTTLVAEKHVLTAACHIDHG 180
 Qy 181 KTVYKGTQKLRVGLPKFPGDGGRGANDSTSAMPEQMKFQWIRKRVTHVPKGMKGNAND 240
 Db 181 KTVYKGTQKLRVGLPKFPGDGGRGANDSTSAMPEQMKFQWIRKRVTHVPKGMKGNAND 240
 Qy 241 IGMDDYVALLLELKKPHRKPKMKIGVSPAPKALPGGRTHFGSYNDNRPNLVYRFDVKDE 300
 Db 241 IGMDDYVALLLELKKPHRKPKMKIGVSPAPKALPGGRTHFGSYNDNRPNLVYRFDVKDE 300
 Qy 301 TYDLLYQCCDAQPCASGSGVYVRMWKQKQKWKRIIGFSGHWDVMDNGSPQDFNVAVR 360
 Db 301 TYDLLYQCCDAQPCASGSGVYVRMWKQKQKWKRIIGFSGHWDVMDNGSPQDFNVAVR 360

Qy 361 ITPLKYAQICYWIKGNLYDCREG 383
 |||||
 Db 361 ITPLKYAQICYWIKGNLYDCREG 383
 |||||
 RESULT 5
 AAY87270
 ID AAY87270 standard; protein; 383 AA.
 XX
 AC AAY87270;
 XX
 DT 11-MAY-2000 (first entry)
 XX
 DE Human signal peptide containing protein HSP-47 SEQ ID NO:47.
 XX
 KW Human; signal peptide-containing protein; HSP; diagnosis; cancer;
 KW inflammation; cardiovascular disease; anticancer; anti-inflammatory;
 KW antimicrobial; nontropic; neuroprotective; cardiovascular; hepatotropic;
 KW antiasthmatic; gene therapy; cell proliferation; neurological disorder;
 KW reproductive disorder; developmental disorder; arteriosclerosis;
 KW cirrhosis; psoriasis; acquired immune deficiency syndrome; anaemia;
 KW asthma; Crohn's disease; infection; Alzheimer's disease; schizophrenia;
 KW Parkinson's disease; Huntington's disease; ovulatory defect;
 KW muscular dystrophy.
 OS Homo sapiens.
 PN WO200000610-A2.
 XX
 PD 06-JAN-2000.
 XX
 PF 25-JUN-1999; 99WO-US014484.
 XX
 PR 26-JUN-1998; 98US-0090762P.
 PR 31-JUL-1998; 98US-0094983P.
 PR 01-OCT-1998; 98US-0102886P.
 PR 11-DEC-1998; 98US-0112129P.
 XX
 PA (INCY-) INCYTE PHARM INC.
 XX
 PI Lal P, Tang YT, Gorgone GA, Corley NC, Guegler KJ, Baughn MR;
 PI Akerbloom IE, Au-Young J, Yue H, Patterson C, Reddy R, Hillman JL;
 PI Bandman O;
 XX
 DR WPI: 2000-160673/14.
 DR N-PSDB; AA298155.
 XX
 PT New human signal peptide-containing proteins useful in treatment,
 PT prevention and diagnosis of e.g. cancer, inflammation and cardiovascular
 PT disease.
 XX
 PS Claim 1; Page 192-193; 327pp; English.
 XX
 CC AA298109 to AA298242 encode AAY87224 to AAY87357 which represent the
 CC human signal peptide-containing proteins HSP-1 to HSP-134. HSPs have
 CC anticancer, anti-inflammatory, antimicrobial, nontropic, hepatotropic,
 CC neuroprotective, cardiovascular and antiasthmatic activities, and can be
 CC used in gene therapy. HSPs can be used to treat or prevent disorders
 CC associated with decreased activity or function of HSP. Antagonists of
 CC HSP are used to treat or prevent disorders associated with increased
 CC activity or function of HSP. Such diseases include cell proliferation
 CC (including cancer), inflammation, cardiovascular, neurological,
 CC reproductive or developmental disorders, (e.g. arteriosclerosis,
 CC cirrhosis, psoriasis, acquired immune deficiency syndrome, anaemia,
 CC asthma, Crohn's disease, microbial or other infections, congestive or
 CC ischaemic heart disease, Alzheimer's, Parkinson's or Huntington's
 CC diseases, schizophrenia, ovulatory defects, muscular dystrophy). HSP
 CC nucleic acids can be used for the recombinant production of HSP, for
 CC detecting HSP in standard hybridisation and amplification assays (for
 CC diagnosis and monitoring), in gene therapy, as antisense, triplex-forming
 CC or ribozyme therapeutics, for detecting related sequences or genetic
 CC variations, and for chromosomal mapping. HSP are also used to raise

CC specific antibodies (Ab) and to screen for agonists and antagonists
CC (potential therapeutic agents). Ab are used to diagnose, or monitor, HSPP
CC -related diseases (in usual immunoassays), as therapeutic antagonists, in
CC competitive drug screens, and for purification of HSPP from natural
CC sources
XX
SQ Sequence 383 AA;
Query Match 100.0%; Score 2080; DB 3; Length 383;
Best Local Similarity 100.0%; Pred. No. 1.8e-145;
Matches 383; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MAGIPGLLFLFFLLCAVGVSPYSAPWKPTWPAIRLPVVLPOSTNLAKPFGAEAKLE 60
Db 1 MAGIPGLLFLFFLLCAVGVSPYSAPWKPTWPAIRLPVVLPOSTNLAKPFGAEAKLE 60
Qy 61 VSSSCGPQCHKGTPPTYBEAKQYLSYETLYANGSRTEQVGIYILSSSGDGAQHRDGS 120
Db 61 VSSSCGPQCHKGTPPTYBEAKQYLSYETLYANGSRTEQVGIYILSSSGDGAQHRDGS 120
Qy 121 SGKSRKRQIYGVDSRFSIFGKDFLLNYPFSTSVKLSGTCTGLVAEKHVLTAACHIDG 180
Db 121 SGKSRKRQIYGVDSRFSIFGKDFLLNYPFSTSVKLSGTCTGLVAEKHVLTAACHIDG 180
Qy 181 KTYVKGTKLRVGLKPKFKDGGRGANDSTSAMPEQMKFQWIRVKTTHVPKGIKGNAND 240
Db 181 KTYVKGTKLRVGLKPKFKDGGRGANDSTSAMPEQMKFQWIRVKTTHVPKGIKGNAND 240
Qy 241 IGMDDYDYLLELKKPKHKKFMKIGVSPPAKQIPGGRIFHSYNDNDRPGNLVYRFDVKDE 300
Db 241 IGMDDYDYLLELKKPKHKKFMKIGVSPPAKQIPGGRIFHSYNDNDRPGNLVYRFDVKDE 300
Qy 301 TYDLYQQCDAPGASGSGVYVVMWKRQOQKWERKIIGIFSGHQMNGSPQDFNVAVR 360
Db 301 TYDLYQQCDAPGASGSGVYVVMWKRQOQKWERKIIGIFSGHQMNGSPQDFNVAVR 360
Qy 361 ITPLKYAQICYWIKGNLYDCREG 383
Db 361 ITPLKYAQICYWIKGNLYDCREG 383
RESULT 6
AAV53627
ID AAY53627 standard; protein; 383 AA.
XX
AC AAY53627;
XX
DT 22-FEB-2000 (first entry)
XX
DE A bone marrow secreted protein designated BMS192.
XX
KW Bone marrow secreted protein; bone marrow stromal cell; cytokine;
KW cell proliferation; cell differentiation; hematopoiesis; anaemia;
KW myeloid cell deficiency; lymphoid cell deficiency; myeloid cell;
KW erythroid progenitor cell; colony stimulating factor; granulocyte;
KW monocyte; macrophage; myelo-suppression; megakaryocyte; platelet;
KW platelet disorder; thrombocytopenia; hematopoietic stem cell;
KW stem cell disorder; aplastic anaemia; bone differentiation;
KW paroxysmal nocturnal hemoglobinuria; bone growth; cartilage; tendon;
KW ligament; nerve; wound healing; tissue repair; burn; incision; ulcer;
KW bone fracture; cartilage damage; artificial joint.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Peptide 1..19
FT /note= "signal peptide"
XX
PN W09933979-A2.
XX
PD 08-JUL-1999.
XX
PF 18-DEC-1998; 98WO-US027008.

XX 30-DEC-1997; 97US-0068958P.
PR 24-SEP-1998; 98US-0101603P.
XX 30-SEP-1998; 98US-0102540P.
XX
PA (CHIR) CHIRON CORP.
XX
PI Lin H, Cao L;
XX
DR WPI; 2000-038344/03.
DR N-PSDB; AA236233.
XX
PT New isolated human polynucleotide and secreted proteins can induce
XX production of other cytokines in certain cell populations.
PS Claim 2; Page 81-82; 120pp; English.
XX
CC AAY53622-43 represent bone marrow secreted proteins of human bone marrow
CC stromal cells. The proteins can exhibit cytokine, cell proliferation, or
CC cell differentiation activity (either inducing or inhibiting). They can
CC be used to support colony forming cells or factor-dependent cell lines,
CC to regulate hematopoiesis, and to treat myeloid or lymphoid cell
CC deficiencies. In addition, they may be used to support the growth and
CC proliferation of erythroid progenitor cells, and to treat various
CC anaemias. They can have colony stimulating factor (CSF) activity and can
CC be used to support the growth and proliferation of myeloid cells such as
CC granulocytes, monocytes or macrophages, to prevent or treat myelo-
CC suppression, to support the growth and proliferation of megakaryocytes
CC and platelets, thereby allowing prevention or treatment of platelet
CC disorders such as thrombocytopenia, to support the growth and
CC proliferation of hematopoietic stem cells, either in place of or in
CC conjunction with platelet transfusions, to treat stem cell disorders,
CC such as aplastic anaemia and paroxysmal nocturnal hemoglobinuria, or to
CC repopulate the stem cell compartment after irradiation or chemotherapy.
CC They can be used for growth or differentiation of bone, cartilage,
CC tendon, ligament, or nerve tissue, as well as for wound healing and
CC tissue repair and replacement, and in the treatment of burns, incisions
CC and ulcers; to induce cartilage and/or bone growth in circumstances where
CC bone is not normally formed and thus have an application in healing bone
CC fractures and cartilage damage or defects, prophylactic use in fracture
CC reduction and also in the improved fixation of artificial joints
XX
SQ Sequence 383 AA;
Query Match 100.0%; Score 2080; DB 3; Length 383;
Best Local Similarity 100.0%; Pred. No. 1.8e-145;
Matches 383; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MAGIPGLLFLFFLLCAVGVSPYSAPWKPTWPAIRLPVVLPOSTNLAKPFGAEAKLE 60
Db 1 MAGIPGLLFLFFLLCAVGVSPYSAPWKPTWPAIRLPVVLPOSTNLAKPFGAEAKLE 60
Qy 61 VSSSCGPQCHKGTPPTYBEAKQYLSYETLYANGSRTEQVGIYILSSSGDGAQHRDGS 120
Db 61 VSSSCGPQCHKGTPPTYBEAKQYLSYETLYANGSRTEQVGIYILSSSGDGAQHRDGS 120
Qy 121 SGKSRKRQIYGVDSRFSIFGKDFLLNYPFSTSVKLSGTCTGLVAEKHVLTAACHIDG 180
Db 121 SGKSRKRQIYGVDSRFSIFGKDFLLNYPFSTSVKLSGTCTGLVAEKHVLTAACHIDG 180
Qy 181 KTYVKGTKLRVGLKPKFKDGGRGANDSTSAMPEQMKFQWIRVKTTHVPKGIKGNAND 240
Db 181 KTYVKGTKLRVGLKPKFKDGGRGANDSTSAMPEQMKFQWIRVKTTHVPKGIKGNAND 240
Qy 241 IGMDDYDYLLELKKPKHKKFMKIGVSPPAKQIPGGRIFHSYNDNDRPGNLVYRFDVKDE 300
Db 241 IGMDDYDYLLELKKPKHKKFMKIGVSPPAKQIPGGRIFHSYNDNDRPGNLVYRFDVKDE 300
Qy 301 TYDLYQQCDAPGASGSGVYVVMWKRQOQKWERKIIGIFSGHQMNGSPQDFNVAVR 360
Db 301 TYDLYQQCDAPGASGSGVYVVMWKRQOQKWERKIIGIFSGHQMNGSPQDFNVAVR 360
Qy 361 ITPLKYAQICYWIKGNLYDCREG 383

Db	361	ITPLKYAQICYWIKGNLYDCREG 383	Query Match 100.0%; Score 2080; DB 3; Length 383; Best Local Similarity 100.0%; Pred. No. 1.8e-145; Matches 383; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
RESULT 7			
AAAB255618			
ID	AAAB255618	standard; protein; 383 AA.	
XX	AAAB255618;		
AC			
XX			
DT	21-NOV-2000	(first entry)	
XX			
DE		Protein encoded by human secreted protein gene #10.	
XX			
KW		Secreted protein; immunosuppressant; anti-inflammatory; antiarthritic;	
KW		antirheumatic; dermatological; antiproliferative; antiarteriosclerotic;	
KW		anticancer; vulnary; antiviral; antibacterial; antifungal;	
KW		immune disorder; Addison's disease; rheumatoid arthritis; dermatitis;	
KW		multiple sclerosis; inflammatory disorder; inflammatory bowel disease;	
KW		Crohn's disease; nephritis; hyperproliferative disorder;	
KW		cardiovascular disorder; coronary arteriosclerosis; myocarditis; cancer;	
KW		melanoma; lymphoma; wound healing; human; chromosome 12.	
XX			
OS		Homo sapiens.	
XX			
PN		WO200029435-A1.	
XX			
PD		25-MAY-2000.	
XX			
PF		27-OCT-1999; 99WO-US025031.	
XX			
PR		28-OCT-1998; 98US-0105971P.	
XX			
PA		(HUMA-) HUMAN GENOME SCI INC.	
XX			
PI		Ni J, Ruben SM, Olsen HS, Young PE, Kenny JJ, Moore PA, Wei Y;	
PI		Greene JM;	
XX			
DR		WPI; 2000-387742/33.	
XX			
XX		Isolated nucleic acid molecules encoding human secreted proteins are used	
PT		for the prevention, amelioration and treatment of autoimmune, cancer,	
PT		inflammatory, hyperproliferative and cardiovascular disorders, cancer,	
PT		wounds, and infectious diseases.	
PS		Disclosure; Page 169; 803pp; English.	
XX			
CC		The present invention relates to 12 secreted human proteins and the	
CC		nucleotide sequences encoding them. The polynucleotide sequences given in	
CC		AAAB0606-A80623 encode the 12 secreted protein sequences given in	
CC		AAAB25576-B25593. The human secreted proteins have various activities	
CC		dependent on the tissues in which they are expressed. Examples of the	
CC		activities of the proteins include: immunosuppressant; anti-inflammatory;	
CC		antiarthritic; antirheumatic; dermatological; antiproliferative;	
CC		antiarteriosclerotic; anticancer; vulnary; antiviral; antibacterial;	
CC		and antifungal activity. The proteins, polypeptides, agonists and	
CC		antagonists may be used to treat prevent and/or diagnose various disease,	
CC		disorders and conditions examples of which include: immune disorders e.g.	
CC		Addison's disease, rheumatoid arthritis, dermatitis, and multiple	
CC		sclerosis; inflammatory disorders e.g. inflammatory bowel disease,	
CC		Crohn's disease and nephritis; hyperproliferative disorders such as	
CC		paraproteinemia and purpura; cardiovascular disorders e.g. coronary	
CC		arteriosclerosis and myocarditis; cancer e.g. melanoma and lymphoma. The	
CC		proteins and polynucleotide sequences may also be used in wound healing	
CC		and the treatment of infectious diseases. The human secreted protein gene	
CC		#10 and protein sequences are represented in sequences AAAB0615 and	
CC		AAAB25585. Secreted protein gene #10 is located on chromosome 12.	
CC		Sequences AAAB25616-B25618 represent alternative secreted protein #10	
CC		sequences and AAAB0669-A80676 represent genes which are related to the	
CC		secreted protein gene#10	
XX			
SQ		Sequence 383 AA;	

QY	1	MAGIPGLLLFLPFLCAVGVSPYSAPWKPPTWPAAYRLPVVLPQSTLNLAKEPFGAEAKLE 60	
DB	1	MAGIPGLLLFLPFLCAVGVSPYSAPWKPPTWPAAYRLPVVLPQSTLNLAKEPFGAEAKLE 60	
QY	61	VSSSCGPGCHKGTPPTLYEAKQYLSYETLYANGSRTEQVGIYIILSSSGDGAQHRDGS 120	
DB	61	VSSSCGPGCHKGTPPTLYEAKQYLSYETLYANGSRTEQVGIYIILSSSGDGAQHRDGS 120	
QY	121	SGKSRKRIQYGYDSRFSIFGKDFILNYPSTSVKLSCTGCTGLVAEKHVLTAACHIDG 180	
DB	121	SGKSRKRIQYGYDSRFSIFGKDFILNYPSTSVKLSCTGCTGLVAEKHVLTAACHIDG 180	
QY	181	KTVVKGTTQLRVGFLKPKFGDGGGANDSTSAMPEQMKFQWIRVKRTHVPKGIKGNAND 240	
DB	181	KTVVKGTTQLRVGFLKPKFGDGGGANDSTSAMPEQMKFQWIRVKRTHVPKGIKGNAND 240	
QY	241	IGMDYDVALLELKKPHKRFMKIGVSPPAKQLPGRHFSGYDNDPRPNIYVYRFDVKDE 300	
DB	241	IGMDYDVALLELKKPHKRFMKIGVSPPAKQLPGRHFSGYDNDPRPNIYVYRFDVKDE 300	
QY	301	TYDLLYQCCDAQPGASGSGYVYRMWKRQOKWKRKIIGIFSGHQWYDMNGSPQDFNVAVR 360	
DB	301	TYDLLYQCCDAQPGASGSGYVYRMWKRQOKWKRKIIGIFSGHQWYDMNGSPQDFNVAVR 360	
QY	361	ITPLKYAQICYWIKGNLYDCREG 383	
DB	361	ITPLKYAQICYWIKGNLYDCREG 383	
RESULT 8			
AAAB25592			
ID	AAAB25592	standard; protein; 383 AA.	
XX			
AC			
XX			
DT	21-NOV-2000	(first entry)	
XX			
DE		Protein encoded by human secreted protein gene #10 clone HUSQ05.	
XX			
KW		Secreted protein; immunosuppressant; anti-inflammatory; antiarthritic;	
KW		antirheumatic; dermatological; antiproliferative; antiarteriosclerotic;	
KW		anticancer; vulnary; antiviral; antibacterial; antifungal;	
KW		immune disorder; Addison's disease; rheumatoid arthritis; dermatitis;	
KW		multiple sclerosis; inflammatory disorder; inflammatory bowel disease;	
KW		Crohn's disease; nephritis; hyperproliferative disorder;	
KW		cardiovascular disorder; coronary arteriosclerosis; myocarditis; cancer;	
KW		melanoma; lymphoma; wound healing; human; chromosome 12.	
XX			
OS		Homo sapiens.	
XX			
PN		WO200029435-A1.	
XX			
PD		25-MAY-2000.	
XX			
PF		27-OCT-1999; 99WO-US025031.	
XX			
PR		28-OCT-1998; 98US-0105971P.	
XX			
PA		(HUMA-) HUMAN GENOME SCI INC.	
XX			
PI		Ni J, Ruben SM, Olsen HS, Young PE, Kenny JJ, Moore PA, Wei Y;	
PI		Greene JM;	
XX			
DR		WPI; 2000-387742/33.	
XX			
XX		Isolated nucleic acid molecules encoding human secreted proteins are used	
PT		for the prevention, amelioration and treatment of autoimmune, cancer,	
PT		inflammatory, hyperproliferative and cardiovascular disorders, cancer,	
PT		wounds, and infectious diseases.	
PS		Disclosure; Page 169; 803pp; English.	
XX			
CC		The present invention relates to 12 secreted human proteins and the	
CC		nucleotide sequences encoding them. The polynucleotide sequences given in	
CC		AAAB0606-A80623 encode the 12 secreted protein sequences given in	
CC		AAAB25576-B25593. The human secreted proteins have various activities	
CC		dependent on the tissues in which they are expressed. Examples of the	
CC		activities of the proteins include: immunosuppressant; anti-inflammatory;	
CC		antiarthritic; antirheumatic; dermatological; antiproliferative;	
CC		antiarteriosclerotic; anticancer; vulnary; antiviral; antibacterial;	
CC		and antifungal activity. The proteins, polypeptides, agonists and	
CC		antagonists may be used to treat prevent and/or diagnose various disease,	
CC		disorders and conditions examples of which include: immune disorders e.g.	
CC		Addison's disease, rheumatoid arthritis, dermatitis, and multiple	
CC		sclerosis; inflammatory disorders e.g. inflammatory bowel disease,	
CC		Crohn's disease and nephritis; hyperproliferative disorders such as	
CC		paraproteinemia and purpura; cardiovascular disorders e.g. coronary	
CC		arteriosclerosis and myocarditis; cancer e.g. melanoma and lymphoma. The	
CC		proteins and polynucleotide sequences may also be used in wound healing	
CC		and the treatment of infectious diseases. The human secreted protein gene	
CC		#10 and protein sequences are represented in sequences AAAB0615 and	
CC		AAAB25585. Secreted protein gene #10 is located on chromosome 12.	
CC		Sequences AAAB25616-B25618 represent alternative secreted protein #10	
CC		sequences and AAAB0669-A80676 represent genes which are related to the	
CC		secreted protein gene#10	
XX			
SQ		Sequence 383 AA;	

XX PS Claim 1; Page 684-685; 803pp; English.

XX CC The present invention relates to 12 secreted human proteins and the

CC nucleotide sequences encoding them. The polynucleotide sequences given in

CC AAB0606-A80623 encode the 12 secreted protein sequences given in

CC AAB25576-B25593. The human secreted proteins have various activities

CC dependent on the tissues in which they are expressed. Examples of the

CC activities of the proteins include: immunosuppressant; anti-inflammatory;

CC antiarthritic; antirheumatic; dermatological; antiproliferative;

CC antiarteriosclerotic; anticancer; vulnerary; antiviral; antibacterial;

CC and antifungal activity. The proteins, polypeptides, agonists and

CC antagonists may be used to treat prevent and/or diagnose various disease.

CC disorders and conditions examples of which include: immune disorders e.g.

CC Addison's disease, rheumatoid arthritis, dermatitis, and multiple

CC sclerosis; inflammatory disorders e.g. inflammatory bowel disease,

CC Crohn's disease and nephritis; hyperproliferative disorders such as

CC paraproteinacemias and purpura; cardiovascular disorders e.g. coronary

CC arteriosclerosis and myocarditis; cancer e.g. melanoma and lymphoma. The

CC proteins and polynucleotide sequences may also be used in wound healing

CC and the treatment of infectious diseases. The human secreted protein gene

CC #10 and protein sequences are represented in sequences AAB0606 and

CC AAB25585. Secreted protein gene #10 is located on chromosome 12.

CC Sequences AAB25616-B25618 represent alternative secreted protein #10

CC sequences and AAB0669-A80676 represent genes which are related to the

CC secreted protein gene#10

XX SQ Sequence 383 AA;

Query Match 100.0%; Score 2080; DB 3; Length 383;

Best Local Similarity 100.0%; Pred. No. 1.8e-145;

Matches 383; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MAGIPGLLLFLLFLLCAVGQVSPYSAPWKPWPAYRLPVVLPQSTLNLAKEPFGAEAKLE 60

Db 1 MAGIPGLLLFLLFLLCAVGQVSPYSAPWKPWPAYRLPVVLPQSTLNLAKEPFGAEAKLE 60

Qy 61 VSSSCGPGQCHKGTPLPTYEAKQVLSYETLYANGSRRTQVGIYILSSSGDGAQHRDGS 120

Db 61 VSSSCGPGQCHKGTPLPTYEAKQVLSYETLYANGSRRTQVGIYILSSSGDGAQHRDGS 120

Qy 121 SGKRRKRQIYGYDSRFSIFGKDFLLNYPFSTSVKLTGCTGTILVAEKHVLTAACHIDG 180

Db 121 SGKRRKRQIYGYDSRFSIFGKDFLLNYPFSTSVKLTGCTGTILVAEKHVLTAACHIDG 180

Qy 181 KTYVKGTKLRVGLKPKFKDGGRGANDSTSAMPEQMKFQWIRVTRTHVPKGIKGNAND 240

Db 181 KTYVKGTKLRVGLKPKFKDGGRGANDSTSAMPEQMKFQWIRVTRTHVPKGIKGNAND 240

Qy 241 IGMDDYALLELKKPKHKKFKMIGVSPPAKQLPGGRIFHSGYDNDPGLNLYRFDVKDE 300

Db 241 IGMDDYALLELKKPKHKKFKMIGVSPPAKQLPGGRIFHSGYDNDPGLNLYRFDVKDE 300

Qy 301 TYDLYOCCDAQPCAGSGGVVVRWKQKQWERKIIFSGHGWDMNGSPQDENVAVR 360

Db 301 TYDLYOCCDAQPCAGSGGVVVRWKQKQWERKIIFSGHGWDMNGSPQDENVAVR 360

Qy 361 ITPLKYAICWIKGNLYDCREG 383

Db 361 ITPLKYAICWIKGNLYDCREG 383

RESULT 9

ADC78573

ID ADC78573

XX CC standard; protein; 383 AA.

XX AC ADC78573;

XX DT 01-JAN-2004 (first entry)

XX DE Human PRO307 protein.

XX KW antiinflammatory; antiulcer; cytostatic; antipsoriatic; antiparkinsonian;

KW nootropic; neuroprotective; vasotropic; chemotactic; angiogenic;

KW neurotrophic; osteopathic; antiasthmatic; antiarthritic; antirheumatic;

KW antiarteriosclerotic; cardiant; antidiabetic; cerebroprotective;

KW thrombolytic; immunomodulator; enterocolitis; Zollinger-Ellison syndrome;

KW gastrointestinal ulceration; psoriasis; cancer; Parkinson's disease;

KW Alzheimer's; ALS; neuropathy; dermal scarring; wound healing;

KW nerve repair; thrombosis; bone; cartilage formation; angiogenesis;

KW asthma; rheumatoid arthritis; multiple sclerosis; inflammatory disorder;

KW atherosclerosis; cardiac injury; infertility; premature aging; AIDS;

KW diabetes; stroke; gene therapy; transgenic; PRO; human.

OS Homo sapiens.

XX WO2000015796-A2.

PN 23-MAR-2000.

XX 15-SEP-1999; 99WO-US021090.

XX 16-SEP-1998; 98WO-US019330.

XX (GETH) GENENTECH INC.

XX Chen J, Goddard A, Gurney AL, Hillan K, Pennica D, Wood WI;

PI Yuan J;

XX WPI; 2000-271434/23.

DR N-PSDB; ADC78572.

XX Novel nucleic acids encoding secreted and transmembrane polypeptides with

PT homology, e.g. to growth and cancer-associated antigens.

XX Claim 12; SEQ ID NO 261; 355pp; English.

XX The invention relates to a novel nucleic acid encoding a PRO polypeptide.

CC The polypeptides and polynucleotides of the invention may be useful as

CC research tools and as therapeutics for treating enterocolitis, Zollinger-

CC Ellison syndrome, gastrointestinal ulceration, psoriasis, cancer,

CC Parkinson's disease, Alzheimer's disease, ALS, neuropathies, dermal

CC scarring and wound healing, nerve repair, thrombosis, bone and/or

CC cartilage formation, angiogenesis, asthma, rheumatoid arthritis, multiple

CC sclerosis, inflammatory disorders, atherosclerosis, cardiac injury,

CC infertility, premature aging, AIDS, diabetes complications and stroke.

CC The molecules may also be utilised during gene therapy procedures and

CC transgenic animal production. The current sequence is that of the human

CC PRO protein of the invention.

XX SQ Sequence 383 AA;

Query Match 100.0%; Score 2080; DB 3; Length 383;

Best Local Similarity 100.0%; Pred. No. 1.8e-145;

Matches 383; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MAGIPGLLLFLLFLLCAVGQVSPYSAPWKPWPAYRLPVVLPQSTLNLAKEPFGAEAKLE 60

Db 1 MAGIPGLLLFLLFLLCAVGQVSPYSAPWKPWPAYRLPVVLPQSTLNLAKEPFGAEAKLE 60

Qy 61 VSSSCGPGQCHKGTPLPTYEAKQVLSYETLYANGSRRTQVGIYILSSSGDGAQHRDGS 120

Db 61 VSSSCGPGQCHKGTPLPTYEAKQVLSYETLYANGSRRTQVGIYILSSSGDGAQHRDGS 120

Qy 121 SGKRRKRQIYGYDSRFSIFGKDFLLNYPFSTSVKLTGCTGTILVAEKHVLTAACHIDG 180

Db 121 SGKRRKRQIYGYDSRFSIFGKDFLLNYPFSTSVKLTGCTGTILVAEKHVLTAACHIDG 180

Qy 181 KTYVKGTKLRVGLKPKFKDGGRGANDSTSAMPEQMKFQWIRVTRTHVPKGIKGNAND 240

Db 181 KTYVKGTKLRVGLKPKFKDGGRGANDSTSAMPEQMKFQWIRVTRTHVPKGIKGNAND 240

Qy 241 IGMDDYALLELKKPKHKKFKMIGVSPPAKQLPGGRIFHSGYDNDPGLNLYRFDVKDE 300

Db 241 IGMDDYALLELKKPKHKKFKMIGVSPPAKQLPGGRIFHSGYDNDPGLNLYRFDVKDE 300

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QY 301 TYDLLYQCCDAQPGASGSGYVVRWKRQKQKWERKIIGIFSGHWDVMDNGSPQDFNVAVR 360
DB 301 TYDLLYQCCDAQPGASGSGYVVRWKRQKQKWERKIIGIFSGHWDVMDNGSPQDFNVAVR 360
QY 361 ITPLKYAQICWIKGNLYDCREG 383
DB 361 ITPLKYAQICWIKGNLYDCREG 383

RESULT 10
AAB80258
ID AAB80258 standard; protein; 383 AA.
XX
AC AAB80258;
XX
DT 24-APR-2001 (first entry)
XX
DE Human PRO307 protein.
XX
KW Human; PRO; dermatological; antipsoriatic; cytostatic; antiinflammatory;
KW antiparkinsonian nootropic; neuroprotective; vulnerary; cardiant;
KW antiangiogenic; vasotropic; antiasthmatic; antirheumatic; cancer;
KW antiarthritic; antinfertility; antidiabetic; antiviral; diabetes;
KW ophthalmological; gene therapy; skin disease; gastrointestinal disorder;
KW ischaemia; inflammation.
XX
OS Homo sapiens.
XX
XX WO200104311-A1.
XX
XX 18-JAN-2001.
XX
XX 22-FEB-2000; 2000WO-US004414.
XX
XX 07-JUL-1999; 99US-0143048P.
XX
XX 26-JUL-1999; 99US-0145698P.
XX
XX 28-JUL-1999; 99US-0146222P.
XX
XX 08-SEP-1999; 99WO-US020594.
XX
XX 13-SEP-1999; 99WO-US020944.
XX
XX 15-SEP-1999; 99WO-US021090.
XX
XX 15-SEP-1999; 99WO-US021547.
XX
XX 05-OCT-1999; 99WO-US023089.
XX
XX 29-NOV-1999; 99WO-US028214.
XX
XX 30-NOV-1999; 99WO-US028313.
XX
XX 02-DEC-1999; 99WO-US028564.
XX
XX 02-DEC-1999; 99WO-US028565.
XX
XX 16-DEC-1999; 99WO-US030095.
XX
XX 20-DEC-1999; 99WO-US030911.
XX
XX 20-DEC-1999; 99WO-US030999.
XX
XX 05-JAN-2000; 2000WO-US000219.
XX
XX (GETH ) GENENTECH INC.
XX
XX Ashkenazi AJ, Botstein D, Desnoyers L, Eaton DL, Ferrara N,
XX Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME, Goddard A,
XX Godowski PJ, Grimaldi CJ, Gurney AL, Hillan KJ, Kljavin IJ,
XX Mather JP, Pan J, Paoni NF, Roy MA, Stewart TA, Tumas D,
XX Williams PM, Wood WI,
XX WPI; 2001-081051/09.
XX
XX N-PSDB; AAF72419.
XX
XX Sixty one nucleic acids encoding PRO polypeptides which are useful in the
XX treatment of skin diseases (e.g. psoriasis), cancers (e.g. lung squamous
XX cell carcinoma) and neurodegenerative diseases (e.g. Alzheimer's
XX disease).
XX
XX Claim 1; Fig 96; 39pp; English.
XX
XX The present sequence is one of sixty one novel secreted and transmembrane
XX PRO polypeptides. The PRO polypeptides are useful for treating skin
XX diseases (e.g. psoriasis), cancers (e.g. lung squamous cell carcinoma),
XX gastrointestinal disorders (e.g. enterocolitis), neurodegenerative
```

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CC diseases (e.g. Alzheimer's disease, Parkinson's disease), wound repair,
CC cardiovascular disorders (e.g. endometrial bleeding angiogenesis,
CC ischaemias such as coronary ischaemia, atherosclerosis), inflammatory
CC disorders (e.g. asthma, rheumatoid arthritis, multiple sclerosis),
CC infertility, AIDS and diabetes and retinal disorders such as retinitis
CC pigmentosum. The PRO nucleic acids have applications in molecular
CC biology, including use as hybridization probes, and in chromosome and
CC gene mapping
XX
XX Sequence 383 AA;
SQ
Query Match 100.0%; Score 2080; DB 4; Length 383;
Best Local Similarity 100.0%; Pred. No. 1.8e-145;
Matches 383; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MAGIPGLLLFLLPFLLCVGVQSPYSAPWKPWPAYRLPVVLPSTLNLAKEPFGAEAKLE 60
DB 1 MAGIPGLLLFLLPFLLCVGVQSPYSAPWKPWPAYRLPVVLPSTLNLAKEPFGAEAKLE 60
QY 61 VSSSCGPGCHKGTPPLTYEEAKQYLSYETLYANGSRTEQVGIYIILSSSGDGAQHRDGS 120
DB 61 VSSSCGPGCHKGTPPLTYEEAKQYLSYETLYANGSRTEQVGIYIILSSSGDGAQHRDGS 120
QY 121 SGKSRKROIYGVDSRFSIFGKDFLLNYPFSTSVKLSGCTGTLVAEKHVLTAACHIDG 180
DB 121 SGKSRKROIYGVDSRFSIFGKDFLLNYPFSTSVKLSGCTGTLVAEKHVLTAACHIDG 180
QY 181 KTVVGTOKLRVGFLLPKFKDGGRGANDSTSAMPEQMKQWIRVKTHTVPKGIKGNAND 240
DB 181 KTVVGTOKLRVGFLLPKFKDGGRGANDSTSAMPEQMKQWIRVKTHTVPKGIKGNAND 240
QY 241 IGMDYDYLLELKKPHKRFKMGKIGVSPPAKQLPGGRIHFSGYDNDPRGNLVYRFDVKDE 300
DB 241 IGMDYDYLLELKKPHKRFKMGKIGVSPPAKQLPGGRIHFSGYDNDPRGNLVYRFDVKDE 300
QY 301 TYDLLYQCCDAQPGASGSGYVVRWKRQKQKWERKIIGIFSGHWDVMDNGSPQDFNVAVR 360
DB 301 TYDLLYQCCDAQPGASGSGYVVRWKRQKQKWERKIIGIFSGHWDVMDNGSPQDFNVAVR 360
QY 361 ITPLKYAQICWIKGNLYDCREG 383
DB 361 ITPLKYAQICWIKGNLYDCREG 383

RESULT 11
AAB48974
ID AAB48974 standard; protein; 383 AA.
XX
AC AAB48974;
XX
XX 27-MAR-2001 (first entry)
XX
XX Human Zsig13 variant #3, SEQ ID NO:18.
XX
XX Human Zsig13; serine protease; chromosome 11q22.1; elastase homologue;
XX glutamyl endopeptidase homologue; factor x homologue; trypsin homologue;
XX trypsinogen homologue; mast cell protease homologue;
XX collagenase homologue; protein degradation; food processing; brewing;
XX alcohol production; laundry detergent component.
XX
XX Homo sapiens.
XX
XX US6153420-A.
XX
XX 28-NOV-2000.
XX
XX 04-MAY-1998; 98US-00072384.
XX
XX 24-APR-1997; 97US-0044185P.
XX
XX 17-APR-1998; 98US-00062142.
XX
XX (ZYMO ) ZYMOGENETICS INC.
XX
```

PI Sheppard PO;
 XX
 DR WPI; 2001-060090/07.
 DR N-PSDB; AAC91784.
 XX
 PT New isolated serine protease (designated Zsig13), useful in industrial
 PT processes to degrade unwanted proteins or alter the characteristics of
 PT protein-containing composition, as well as in industrial applications
 PT (e.g. brewing).
 XX
 XX Claim 1; Col 41-44; 26pp; English.
 XX
 CC The invention relates to human Zsig13 proteins (AAB48972-B48974), and to
 CC DNA encoding them (AAC91782-C91784). The invention also relates to
 CC expression vectors and host cells comprising a human Zsig13 DNA, and the
 CC recombinant production of a human Zsig13 protein or its precursor. Zsig13
 CC is a serine protease, and has significant homology to Bacillus
 CC licheniformis glutamyl endopeptidase, human clotting factor X, human
 CC elastase, rat mast cell protease, Streptomyces griseus trypsin, bovine
 CC trypsinogen, and Hypoderma lineatum collagenase. The gene encoding human
 CC Zsig13 is located on chromosome 11q22.1. Zsig13 is useful in industrial
 CC processes to degrade unwanted proteins or alter the characteristics of
 CC protein-containing compositions. It may also be used in industrial
 CC applications in which proteases are utilized, including food processing,
 CC brewing and alcohol production, and as a component of a laundry
 CC detergent. The present sequence represents a human Zsig13 variant
 XX
 XX Sequence 383 AA;
 SQ
 Query Match 100.0%; Score 2080; DB 4; Length 383;
 Best Local Similarity 100.0%; Pred. No. 1.8e-145;
 Matches 383; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MAGIPGLLFLFLLCVAGQVSPYSAPKPTPAYRLPVVLPSTLNLAKEPFGAEAKLE 60
 Db 1 MAGIPGLLFLFLLCVAGQVSPYSAPKPTPAYRLPVVLPSTLNLAKEPFGAEAKLE 60
 QY 61 VSSSCGPGCHGTPLPTYPEAKQVLSYETLYANGSRRTETQVGIYILSSSGDGAQHRDGS 120
 Db 61 VSSSCGPGCHGTPLPTYPEAKQVLSYETLYANGSRRTETQVGIYILSSSGDGAQHRDGS 120
 QY 121 SGKRRKQIYGVDSRFSIFGKDFLLNYPSTSVKLTSTGCTGLVAEKHVLTAHCHIDG 180
 Db 121 SGKRRKQIYGVDSRFSIFGKDFLLNYPSTSVKLTSTGCTGLVAEKHVLTAHCHIDG 180
 QY 181 KTVKGTQKLRVGLFKPKFDDGGRGANDSTSAPEQMKFQIRVKTTHVPKGIKGNAND 240
 Db 181 KTVKGTQKLRVGLFKPKFDDGGRGANDSTSAPEQMKFQIRVKTTHVPKGIKGNAND 240
 QY 241 IGMDDYVALLLELKKPKRKFPMKIGVSPPAKQLPGRIHFSGYNDNRPNLVYRFDVKDE 300
 Db 241 IGMDDYVALLLELKKPKRKFPMKIGVSPPAKQLPGRIHFSGYNDNRPNLVYRFDVKDE 300
 QY 301 TYDLLVOCCDAOPGASGVYVVRWKKQKQKWKRIIGIFSGHWDVDMGSPQDENVAVR 360
 Db 301 TYDLLVOCCDAOPGASGVYVVRWKKQKQKWKRIIGIFSGHWDVDMGSPQDENVAVR 360
 QY 361 ITPKVAQICWIKGNVLDREG 383
 Db 361 ITPKVAQICWIKGNVLDREG 383
 RESULT 12.
 AAU29048
 ID AAU29048 standard; protein; 383 AA.
 XX
 AC AAU29048;
 XX
 DT 18-DEC-2001 (first entry)
 XX
 DE Human PRO polypeptide sequence #25.
 XX
 XX PRO polypeptide; mammal; tumour; cancer; human; cattle; horse; sheep;

KW dog; cat; pig; goat; rabbit; tumour necrosis factor alpha; TNF-alpha;
 KW blood; chondrocyte cell; cell proliferation; cell differentiation; colon;
 KW adrenal; lung; breast; prostate; rectum; cervix; liver; genetic disorder.
 XX
 OS Homo sapiens.
 XX
 PN WO200168848-A2.
 XX
 PD 20-SEP-2001.
 XX
 XX 28-FEB-2001; 2001WO-US006520.
 XX
 XX 01-MAR-2000; 2000WO-US005601.
 PR 02-MAR-2000; 2000WO-US005841.
 PR 03-MAR-2000; 2000US-0187202P.
 PR 06-MAR-2000; 2000US-0186968P.
 PR 14-MAR-2000; 2000US-0189320P.
 PR 14-MAR-2000; 2000US-0189328P.
 PR 15-MAR-2000; 2000WO-US006884.
 PR 21-MAR-2000; 2000US-0190828P.
 PR 21-MAR-2000; 2000US-0191007P.
 PR 21-MAR-2000; 2000US-0191048P.
 PR 21-MAR-2000; 2000US-0191314P.
 PR 28-MAR-2000; 2000US-0192655P.
 PR 29-MAR-2000; 2000US-0193032P.
 PR 29-MAR-2000; 2000US-0193053P.
 PR 30-MAR-2000; 2000WO-US008439.
 PR 04-APR-2000; 2000US-0194449P.
 PR 04-APR-2000; 2000US-0194647P.
 PR 11-APR-2000; 2000US-0195975P.
 PR 11-APR-2000; 2000US-0196000P.
 PR 11-APR-2000; 2000US-0196187P.
 PR 11-APR-2000; 2000US-0196690P.
 PR 11-APR-2000; 2000US-0196820P.
 PR 18-APR-2000; 2000US-0198121P.
 PR 18-APR-2000; 2000US-0198585P.
 PR 25-APR-2000; 2000US-0199397P.
 PR 25-APR-2000; 2000US-0199550P.
 PR 25-APR-2000; 2000US-0199654P.
 PR 03-MAY-2000; 2000US-0201516P.
 PR 17-MAY-2000; 2000WO-US013705.
 PR 22-MAY-2000; 2000WO-US014042.
 PR 30-MAY-2000; 2000WO-US014941.
 PR 02-JUN-2000; 2000WO-US015264.
 PR 05-JUN-2000; 2000US-0209832P.
 PR 28-JUL-2000; 2000WO-US020710.
 PR 22-AUG-2000; 2000US-00644848.
 PR 24-AUG-2000; 2000WO-US023328.
 PR 08-NOV-2000; 2000WO-US030952.
 PR 01-DEC-2000; 2000WO-US032678.
 PR 20-DEC-2000; 2000WO-US034956.
 XX
 (GETH) GENENTECH INC.
 PA
 XX Baker KP, Chen J, Desnoyers L, Goddard A, Godowski PJ, Gurney AL;
 PI Pan J, Smith V, Watanabe CK, Wood WI, Zhang Z;
 XX
 XX WPI; 2001-602746/68.
 DR N-PSDB; AAS45949.
 XX
 XX Novel nucleic acids encoding PRO polypeptides, used to diagnose the
 PT presence of tumors, such as prostate and breast tumors, in mammals and to
 PT screen for modulators of the compounds.
 XX
 XX Claim 11; Fig 50; 774pp; English.
 PS
 XX Sequences AAU29024-AAU29328 represent PRO polypeptides of the invention.
 CC The PRO polypeptides and their associated nucleic acids can be used to
 CC detect the presence of a tumour in a mammal by comparing the level of
 CC expression of a PRO polypeptide in a test sample of cells from the animal
 CC and a control sample of normal cells, whereby a higher level of
 CC expression in the test sample indicates the presence of a tumour in the
 CC mammal. Mammals include dogs, cats, cattle, horses, sheep, pigs, goats


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PR 11-JUN-1998; 98US-0088861P.
PR 11-JUN-1998; 98US-0088863P.
PR 11-JUN-1998; 98US-0088876P.
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PR 16-JUN-1998; 98US-0089512P.
PR 16-JUN-1998; 98US-0089514P.
PR 17-JUN-1998; 98US-0089538P.
PR 17-JUN-1998; 98US-0089598P.
PR 17-JUN-1998; 98US-0089633P.
PR 18-JUN-1998; 98US-0089908P.
PR 19-JUN-1998; 98US-0089952P.
PR 22-JUN-1998; 98US-0090246P.
PR 22-JUN-1998; 98US-0090252P.
PR 22-JUN-1998; 98US-0090254P.
PR 24-JUN-1998; 98US-0090429P.
PR 24-JUN-1998; 98US-0090435P.
PR 24-JUN-1998; 98US-0090444P.
PR 24-JUN-1998; 98US-0090461P.
PR 24-JUN-1998; 98US-0090535P.
PR 24-JUN-1998; 98US-0090540P.
PR 25-JUN-1998; 98US-0090676P.
PR 25-JUN-1998; 98US-0090678P.
PR 25-JUN-1998; 98US-0090688P.
PR 25-JUN-1998; 98US-0090690P.
PR 25-JUN-1998; 98US-0090694P.
PR 25-JUN-1998; 98US-0090695P.
PR 26-JUN-1998; 98US-0090696P.
PR 26-JUN-1998; 98US-00105413.
PR 26-JUN-1998; 98US-0090862P.
PR 26-JUN-1998; 98US-0090863P.
PR 26-JUN-1998; 98US-0091010P.
PR 01-JUL-1998; 98US-0091359P.
PR 01-JUL-1998; 98US-0091544P.
PR 02-JUL-1998; 98US-0091478P.
PR 02-JUL-1998; 98US-0091486P.
PR 02-JUL-1998; 98US-0091626P.
PR 02-JUL-1998; 98US-0091628P.
PR 02-JUL-1998; 98US-0091632P.
PR 28-JUL-1998; 98US-0094006P.
PR 04-AUG-1998; 98US-0095282P.
PR 10-AUG-1998; 98US-0095998P.
PR 10-AUG-1998; 98US-0096012P.
PR 17-AUG-1998; 98US-0096757P.
PR 17-AUG-1998; 98US-0096766P.
PR 17-AUG-1998; 98US-0096867P.
PR 17-AUG-1998; 98US-0096891P.
PR 17-AUG-1998; 98US-0096897P.
PR 18-AUG-1998; 98US-0096949P.
PR 18-AUG-1998; 98US-0096959P.
PR 18-AUG-1998; 98US-0097022P.
PR 26-AUG-1998; 98US-0097952P.
PR 26-AUG-1998; 98US-0097954P.
PR 26-AUG-1998; 98US-0097955P.
PR 26-AUG-1998; 98US-0097971P.
PR 26-AUG-1998; 98US-0097974P.
PR 26-AUG-1998; 98US-0098014P.
PR 01-SEP-1998; 98US-0098716P.
PR 01-SEP-1998; 98US-0098723P.
PR 02-SEP-1998; 98US-0098803P.
PR 02-SEP-1998; 98US-0098821P.
PR 02-SEP-1998; 98US-0098843P.
PR 09-SEP-1998; 98US-0099602P.
PR 10-SEP-1998; 98US-0099741P.
PR 10-SEP-1998; 98US-0099754P.
PR 10-SEP-1998; 98US-0099763P.
PR 10-SEP-1998; 98US-0099812P.
PR 15-SEP-1998; 98US-0100388P.
PR 16-SEP-1998; 98US-0100662P.
PR 16-SEP-1998; 98US-0100664P.
PR 16-SEP-1998; 98US-0101751P.
PR 16-SEP-1998; 98MO-US019330.
PR 17-SEP-1998; 98US-0100683P.

PR 17-SEP-1998; 98US-0100684P.
PR 17-SEP-1998; 98US-0100919P.
PR 17-SEP-1998; 98US-0100930P.
PR 18-SEP-1998; 98US-0100849P.
PR 18-SEP-1998; 98US-0101014P.
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PR 25-SEP-1998; 98US-0101786P.
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PR 01-OCT-1998; 98US-0102684P.
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PR 02-OCT-1998; 98US-0102965P.
PR 06-OCT-1998; 98US-0103258P.
PR 06-OCT-1998; 98US-0103449P.
PR 07-OCT-1998; 98US-00168978.

Query Match 100.0%; Score 2080; DB 6; Length 383;
Best Local Similarity 100.0%; Pred. No. 1.8e-145;
Matches 383; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 241 IGMDYDYLLELKKPKFKMKGVSPPAKQLPGGRIHFSGYDNDPRGNLVYRFDVKDE 300
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Qy 301 TYDLLYQQCDAQPGASGSGVYVRMWKQKQKWERKIIGIFSGHQWVDMNGSPQDFNVAVR 360
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Qy 361 ITELKVAQICYWIKGNLYDCREG 383
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XX 16-JUN-2003 (first entry)
XX Human PRO polypeptide #47.
XX Human; PRO; secreted polypeptide; transmembrane polypeptide;
KW
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ID ABUS87972 standard; protein; 383 AA.
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XX 07-JUL-2003 (first entry)
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XX Human; secreted and transmembrane protein: PRO; gene therapy;
KW tumour necrosis factor-alpha release; TNF-alpha release;
KW chondrocyte proliferation; chondrocyte differentiation; tumour;
KW adrenal tumour; lung tumour; colon tumour; breast tumour;
KW prostate tumour; rectal tumour; cervical tumour; liver tumour.
XX
XX Homo sapiens.
XX
XX US2003032127-A1.
XX
XX 13-FEB-2003.
XX
XX 26-JUN-2002; 2002US-00183012.
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XX 18-SEP-1997; 97US-0059263P.
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XX 25-JUN-1998; 98US-0090694P.
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GenCore version 5.1.6
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OM protein - protein search, using sw model

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1102.727 Million cell updates/sec

Title: US-09-658-677-18

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Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	2080	100.0	383	4	US-09-902-775A-261
5	2080	100.0	383	4	US-09-906-700-261
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14	193	9.3	316	4	US-09-551-826D-2
15	177	8.5	222	1	US-08-090-048-1
16	177	8.5	222	2	US-08-292-550-1
17	177	8.5	222	2	US-07-927-661A-1
18	176.5	8.5	318	4	US-09-551-826D-10
19	140.5	6.8	239	4	US-09-107-433-3471
20	135.5	6.5	313	4	US-09-551-826D-14
21	132	6.3	218	4	US-09-583-110-3950
22	129.5	6.2	302	4	US-09-551-826D-12
23	129	6.2	433	4	US-09-949-016-8220
24	127	6.1	303	4	US-09-551-826D-8
25	127	6.1	320	4	US-09-489-039A-13989
26	126.5	6.1	356	4	US-09-902-540-12881
27	122.5	5.9	238	4	US-09-664-595A-15

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Sequence 32, Appl
Sequence 89, Appl
Sequence 89, Appl
Sequence 7, Appl
Sequence 7, Appl
Sequence 7, Appl
Sequence 2, Appl
Sequence 59, Appl
Sequence 44, Appl
Patent No. 5223425
Patent No. 5223425
Patent No. 5223425

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29 122 5.9 256 3 US-08-906-616-89
30 122 5.9 256 3 US-08-817-795-89
31 122 5.9 256 3 US-08-639-075A-89
32 122 5.9 256 3 US-09-012-431-89
33 122 5.9 256 3 US-09-032-215-32
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38 120 5.8 284 4 US-10-041-400A-7
39 120 5.8 284 4 US-10-042-091A-7
40 117 5.6 437 1 US-08-487-037-2
41 115.5 5.6 241 3 US-08-944-483-59
42 114 5.5 228 3 US-08-944-483-44
43 114 5.5 253 6 5223425-8
44 114 5.5 253 6 5223425-8
45 113 5.4 238 6 5223425-5

ALIGNMENTS

RESULT 1
US-09-072-384-18
; Sequence 18, Application US/09072384
; Patent No. 6153420
; GENERAL INFORMATION:
; APPLICANT: Sheppard, Paul O.
; TITLE OF INVENTION: SERINE PROTEASE POLYPEPTIDES
; AND MATERIALS AND METHODS FOR MAKING THEM
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSSEE: ZymoGenetics, Inc.
; STREET: 1201 Eastlake Avenue East
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98102
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/072,384
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Parker, Gary E
; REGISTRATION NUMBER: 31,648
; REFERENCE/DOCKET NUMBER: 97-16C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-442-6673
; TELEFAX: 206-442-6678
; TELEX:
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 383 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
; FEATURE:
; NAME/KEY: Signal Sequence
; LOCATION: 1...19
; OTHER INFORMATION:
; US-09-072-384-18

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US-09-907-794A-261

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: Sequence 261, Application US/09907794A
: Patent No. 6635468
: GENERAL INFORMATION:
: APPLICANT: Genentech, Inc.
: APPLICANT: Ashkenazi, Avi
: APPLICANT: Botstein, David
: APPLICANT: Desnovers, Luc
: APPLICANT: Eaton, Dan L.
: APPLICANT: Ferrara, Napoleone
: APPLICANT: Filvaroff, Ellen
: APPLICANT: Fong, Sherman
: APPLICANT: Gao, Wei-Qiang
: APPLICANT: Gerber, Hanspeter
: APPLICANT: Gerritsen, Mary E.
: APPLICANT: Goddard, A.
: APPLICANT: Godowski, Carl J.
: APPLICANT: Grimaldi, Christopher J.
: APPLICANT: Gurney, Austin L.
: APPLICANT: Hillan, Kenneth, J.
: APPLICANT: Kljavin, Ivar J.
: APPLICANT: Mather, Jennie P.
: APPLICANT: Pan, James
: APPLICANT: Paoni, Nicholas P.
: APPLICANT: Roy, Margaret Ann
: APPLICANT: Stewart, Timothy A.
: APPLICANT: Tumas, Daniel
: APPLICANT: Williams, P. Mickey
: APPLICANT: Wood, William, I.
: TITLE OF INVENTION: Secreted and Transferred
: TITLE OF INVENTION: Acids Encoding the
: FILE REFERENCE: 10466-14
: CURRENT APPLICATION NUMBER: US/09/907794
: CURRENT FILING DATE: 2001-07-17
: PRIOR APPLICATION NUMBER: PCT/US00/04466
: PRIOR FILING DATE: 2000-08-22
: PRIOR APPLICATION NUMBER: US 60/143,000
: PRIOR FILING DATE: 1999-07-07
: PRIOR APPLICATION NUMBER: US 60/145,616

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RESULT 3

US-09-905-125A-261

; Sequence 261, Application US/09905125A

; Patent No. 6664376

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? PRIOR FILING DATE: 1999-07-26
? PRIOR APPLICATION NUMBER: US 60/146,222
? PRIOR FILING DATE: 1999-07-28
? PRIOR APPLICATION NUMBER: PCT/US99/20594
? PRIOR FILING DATE: 1999-09-08
? PRIOR APPLICATION NUMBER: PCT/US99/20944
? PRIOR FILING DATE: 1999-09-13
? PRIOR APPLICATION NUMBER: PCT/US99/21090
? PRIOR FILING DATE: 1999-09-15
? PRIOR APPLICATION NUMBER: PCT/US99/21547
? PRIOR FILING DATE: 1999-09-15
? PRIOR APPLICATION NUMBER: PCT/US99/23089
? PRIOR FILING DATE: 1999-10-05
? PRIOR APPLICATION NUMBER: PCT/US99/28214
? PRIOR FILING DATE: 1999-11-29
? PRIOR APPLICATION NUMBER: PCT/US99/28313
? PRIOR FILING DATE: 1999-11-30
? PRIOR APPLICATION NUMBER: PCT/US99/28564
? PRIOR FILING DATE: 1999-12-02
? PRIOR APPLICATION NUMBER: PCT/US99/28565
? PRIOR FILING DATE: 1999-12-02
? PRIOR APPLICATION NUMBER: PCT/US99/30095
? PRIOR FILING DATE: 1999-12-16
? PRIOR APPLICATION NUMBER: PCT/US99/30911
? PRIOR FILING DATE: 1999-12-20
? PRIOR APPLICATION NUMBER: PCT/US99/30999
? PRIOR FILING DATE: 1999-12-20
? PRIOR APPLICATION NUMBER: PCT/US00/00219
? PRIOR FILING DATE: 2000-01-05
? NUMBER OF SEQ ID NOS: 423
? SEQ ID NO 261
? LENGTH: 383
? TYPE: PRT
? ORGANISM: Homo Sapien
? US-09-907-794A-261

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Query Match 100.0%: Score 2080: DB 4: Length 383:

Query MacCm 100.0%; SCORE 2080; DB 4; Length 363;
Best Local Similarity 100.0%; Pred No 5 4e-220.

BEST LOCAL SIMILARITY 100.0%; PRED. NO. 3.4E-220;
Matches 383: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

Qy	1	MAGIPGLLFLFLFLLCAVGQVSPYSAPWKPTWPAYRLPVVLTPOSTLNIAKPDFGAEAKLE	60
D6	1	MAGIPGLLFLFLFLLCAVGQVSPYSAPWKPTWPAYRLPVVLTPOSTLNIAKPDFGAEAKLE	60

QY 61 VSSCGPQCHKGTPDPTYEAKQYLSVETLYANGSRTEQTQVGIYILSSSGDCAQHRDGS 120

Db 61 VSSCGPQCHKGTPLPTYEAAKQYLSYETLYANGSRRTQTQVIYILSSSGDGAQHRDSSG 120

QY 121 SGKSRKRQIYGYDSRPSIFGKDFLLNYPFSTSVKLSCTGCTGLVAEKHVLTAACIHDG 180

Db 121 SGKSRKRQIYGYDSRFSIFGKDFLLNYPFSTVKLSTGTGTLVAEKHVI.TAAHC.IHDG 180

QY 181 KTYVKGTOQLRVGFFLKPFPKDGGRGANDSTSAIPEOMKFQWIRVCRTHVPKGIKGNAND 240

Db 181 KTYVKGTKLRVGFLLPKFKDGGRGANDSTANPEQMKQWIRVTRTHVPKGWIKGNAND 240

QY 241 IGMDYDYLLELKKPHKRFMKIGVSPAKQLFGRIFHESGYDNDRPGNLVYRFCDVKDE 300

Db 241 IGMDYDALLELEKKPHKRFMKIGVSPAKQLPGGRIFHESGYDNDRPGNLVYRFCDVKDE 300

Qy 301 TYDLLYQQCDAPGASGSGVYVRWKRRQQQKWERKIIGIFSGHQVYDMNGSPQDFNVAVR 360

Db 301 TYDLLYQQCDAQPGASGSGVYVRMKRQQKWERKIIGIFSGHQWYDMNGSPQDFNVAVR 360

Qy 361 ITPLKYAQICYWIKGNLYDCREG 383

Db 361 ITPLKYAQICYWIKGNYLDCREG 383

RESULT 3

US-09-905-125A-261
; Sequence 261, Application US/09905125A

; Patent No. 6664376

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; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Deenoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/905,125A
; CURRENT FILING DATE: 2001-07-12
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 261
; LENGTH: 383
; TYPE: PRT
; ORGANISM: Homo Sapien
; US-09-905-125A-261
; Query Match 100.0%; Score 2080; DB 4; Length 383;

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Best Local Similarity 100.0%; Pred. No. 5.4e-220;
Matches 383; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MAGIPGLLLFLFLCAVGQVSPYSAPWKPTWPAYRLPVVLPOSTLNLAKPDPFGAEAKLE 60
Db 1 MAGIPGLLLFLFLCAVGQVSPYSAPWKPTWPAYRLPVVLPOSTLNLAKPDPFGAEAKLE 60
Qy 61 VSSSCGPGQCHKGTPLPYEEAKOYLSYETLYANGSRRTETQVGIYILSSSGDGAQHRDGS 120
Db 61 VSSSCGPGQCHKGTPLPYEEAKOYLSYETLYANGSRRTETQVGIYILSSSGDGAQHRDGS 120
Qy 121 SGKSRKRQIYGYDSRFSIFGKDFLLNYPFSTSVKLTGTGTLVAEKHVLTAACHIDG 180
Db 121 SGKSRKRQIYGYDSRFSIFGKDFLLNYPFSTSVKLTGTGTLVAEKHVLTAACHIDG 180
Qy 181 KTVYKGTQKLRVGFPLKPKFGDGGRGANDSTSAPEQMKFQWIRVKTHTVPKGTWKNAND 240
Db 181 KTVYKGTQKLRVGFPLKPKFGDGGRGANDSTSAPEQMKFQWIRVKTHTVPKGTWKNAND 240
Qy 241 IGMDDYVALLLELKKPKHKFKMKIGVSPKQLPGRIFHSGYDNDNRPGNLVYRCDVKDE 300
Db 241 IGMDDYVALLLELKKPKHKFKMKIGVSPKQLPGRIFHSGYDNDNRPGNLVYRCDVKDE 300
Qy 301 TYDLLYQQCDAQPCASGSGVYVVMWKRQQQKWKRIIGIFSGHQMVDNMGSPQDFNVAVR 360
Db 301 TYDLLYQQCDAQPCASGSGVYVVMWKRQQQKWKRIIGIFSGHQMVDNMGSPQDFNVAVR 360
Qy 361 ITPLKVAQICYWIKNYLDCREG 383
Db 361 ITPLKVAQICYWIKNYLDCREG 383

RESULT 4
US-09-902-775A-261
; Sequence 261, Application US/09902775A
; Patent No. 6686451
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Deenoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/902,775A
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26

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Matches	383;	Conservative	0;	Mismatches	0;	Indels	0;	Gaps	0;
Qy	1	MAGIPGLLFLFFLLCAVGQSPISAPWKPTWPAYRLPVVLPOSTLNLAKPDFGAEA	60						
Db	1	MAGIPGLLFLFFLLCAVGQSPISAPWKPTWPAYRLPVVLPOSTLNLAKPDFGAEA	60						
Qy	61	VSSCGPQCHKGTPLPTYEEAKQLSYETLLYANGSRSTETQVGIYILSSGSGAQRHDS	120						
Db	61	VSSCGPQCHKGTPLPTYEEAKQLSYETLLYANGSRSTETQVGIYILSSGSGAQRHDS	120						
Qy	121	SGKRRKRQIYGYDSRFSIFGKDFLLNYPFSTSVKLSGTGCTGLVAEKHVLTAACHIDG	180						
Db	121	SGKRRKRQIYGYDSRFSIFGKDFLLNYPFSTSVKLSGTGCTGLVAEKHVLTAACHIDG	180						
Qy	181	KTYVKGQTKLRVGLKPKFKDGGRGANDSTSAMPEQMKFQWIRVKRTHVPKGIKGNAND	240						
Db	181	KTYVKGQTKLRVGLKPKFKDGGRGANDSTSAMPEQMKFQWIRVKRTHVPKGIKGNAND	240						
Qy	241	IGMDYDVALLELKKPHKPKFKMIIGVSPPAKQLPGRIFHSGYDNDRPGNLVYRFCDVKDE	300						
Db	241	IGMDYDVALLELKKPHKPKFKMIIGVSPPAKQLPGRIFHSGYDNDRPGNLVYRFCDVKDE	300						
Qy	301	TYDILLYQCCDAQPGASGSGVYVRWVKRQQQKWERKIIGIPSGHQWDMNGSPQDFNVAVR	360						
Db	301	TYDILLYQCCDAQPGASGSGVYVRWVKRQQQKWERKIIGIPSGHQWDMNGSPQDFNVAVR	360						
Qy	361	ITPLKYAQICWIKGNVLDREG	383						
Db	361	ITPLKYAQICWIKGNVLDREG	383						

RESULT 6

US/09-903-603A-261
; Sequence 261, Application US/09903603A
; Patent No. 676795
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnovers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: GNE.1618P2C12
; CURRENT APPLICATION NUMBER: US/09/903,603A
; CURRENT FILING DATE: 2001-07-11
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222

RESIN.T 7

US-09-904-920A-261
; Sequence 261, Application US/09904920A
; Patent No. 6806352
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.

APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, A.
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, Christopher J.
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth, J.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Mather, Jennie P.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: 10466-14
CURRENT APPLICATION NUMBER: US/09/904,920A
PRIOR FILING DATE: 2001-07-13
PRIOR APPLICATION NUMBER: PCT/US00/04414
PRIOR FILING DATE: 2000-02-22
PRIOR APPLICATION NUMBER: US 60/143,048
PRIOR FILING DATE: 1999-07-07
PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR FILING DATE: 1999-07-26
PRIOR APPLICATION NUMBER: US 60/146,222
PRIOR FILING DATE: 1999-07-28
PRIOR APPLICATION NUMBER: PCT/US99/20594
PRIOR FILING DATE: 1999-09-08
PRIOR APPLICATION NUMBER: PCT/US99/20944
PRIOR FILING DATE: 1999-09-13
PRIOR APPLICATION NUMBER: PCT/US99/21090
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/21547
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/23089
PRIOR FILING DATE: 1999-10-05
PRIOR APPLICATION NUMBER: PCT/US99/28214
PRIOR FILING DATE: 1999-11-29
PRIOR APPLICATION NUMBER: PCT/US99/28313
PRIOR FILING DATE: 1999-11-30
PRIOR APPLICATION NUMBER: PCT/US99/28364
PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/28565
PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/30095
PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: PCT/US99/30911
PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US99/30999
PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US00/00219
PRIOR FILING DATE: 2000-01-05
NUMBER OF SEQ ID NOS: 423
SEQ ID NO 261
LENGTH: 383
TYPE: PRT
ORGANISM: Homo Sapien
US-09-904-920A-261
Query Match 100.0%; Score 2080; DB 4; Length 383;
Best Local Similarity 100.0%; Pred. No. 5.4e-220;
Matches 383; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAGIPGLLFLFLLCAVGVSPYSAPWKPTWPAYRLPVVLPOSTLNLAKPFGAEAKLE 60
DB 1 MAGIPGLLFLFLLCAVGVSPYSAPWKPTWPAYRLPVVLPOSTLNLAKPFGAEAKLE 60
QY 61 VSSSCGPOCHKGTPLTYEAKQYLSYETLYANGSRTETQVGIYIILSSGSGAQRHDSGS 120
DB 61 VSSSCGPOCHKGTPLTYEAKQYLSYETLYANGSRTETQVGIYIILSSGSGAQRHDSGS 120
QY 121 SGKSRKROIYGYDSRFSIFGKDFLLNYPFSTSVKLSCTGTGLVAEKHVLTAACHIDG 180
DB 121 SGKSRKROIYGYDSRFSIFGKDFLLNYPFSTSVKLSCTGTGLVAEKHVLTAACHIDG 180
QY 181 KTVVKGTKLRVGFLLKPKFKDGGRGANDSTSAMPEQMKFQWIRVKRTHVPKGIKGNAND 240
DB 181 KTVVKGTKLRVGFLLKPKFKDGGRGANDSTSAMPEQMKFQWIRVKRTHVPKGIKGNAND 240
QY 241 IGMDDYALLELKKPHKRFKMGIVSPPAKQLPGGRIHFSGYDNDPRGNLVRFCVKDE 300
DB 241 IGMDDYALLELKKPHKRFKMGIVSPPAKQLPGGRIHFSGYDNDPRGNLVRFCVKDE 300
QY 301 TYDLLVQOCDAOPGASGSGVYVVMWKRQCKWKRIIGIFSGHGWVDMNGSPQDFNVAVR 360
DB 301 TYDLLVQOCDAOPGASGSGVYVVMWKRQCKWKRIIGIFSGHGWVDMNGSPQDFNVAVR 360
QY 361 ITPLKYAQICYWIKGNLYDCREG 383
DB 361 ITPLKYAQICYWIKGNLYDCREG 383
RESULT 8
US-09-909-064-261
Sequence 261, Application US/09909064
Patent No. 6818449
GENERAL INFORMATION:
APPLICANT: Genentech, Inc.
APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, A.
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, Christopher J.
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth, J.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Mather, Jennie P.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: 10466-14
CURRENT APPLICATION NUMBER: US/09/909,064
PRIOR FILING DATE: 2001-07-18
PRIOR APPLICATION NUMBER: PCT/US00/04414
PRIOR FILING DATE: 2000-02-22
PRIOR APPLICATION NUMBER: US 60/143,048
PRIOR FILING DATE: 1999-07-07
PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR FILING DATE: 1999-07-26
PRIOR APPLICATION NUMBER: US 60/146,222
PRIOR FILING DATE: 1999-07-28

; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 261
; LENGTH: 383
; TYPE: PRT
; ORGANISM: Homo Sapien
US-09-909-064-261

Query Match 100.0%; Score 2080; DB 4; Length 383;
Best Local Similarity 100.0%; Pred. No. 5.4e-220;
Matches 383; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MAGIPGLLFLFLLCAGVQSPVSPAPKPTWPAYRLPVVLPSTLNLAKEPFGAEAKLE 60
Db 1 MAGIPGLLFLFLLCAGVQSPVSPAPKPTWPAYRLPVVLPSTLNLAKEPFGAEAKLE 60

Qy 61 VSSSCGQCHKGTPLYEBAKQVLSYETLYANGSRRTQVGIYILSSGSGAQHRDGS 120
Db 61 VSSSCGQCHKGTPLYEBAKQVLSYETLYANGSRRTQVGIYILSSGSGAQHRDGS 120

Qy 121 SGSRKRRQIYGVDSRFSIFGKDFLLNYPSTSVKLTGCTGLVAEKHVLTAACHIDG 180
Db 121 SGSRKRRQIYGVDSRFSIFGKDFLLNYPSTSVKLTGCTGLVAEKHVLTAACHIDG 180

Qy 181 KTVVGTOKLVGFLKPKFVGGGANDSTSAMPEQMKFQWIRKTRHVPKGIKGNAND 240
Db 181 KTVVGTOKLVGFLKPKFVGGGANDSTSAMPEQMKFQWIRKTRHVPKGIKGNAND 240

Qy 241 IGMDDYDVALLEKPKHKKFMKIGVSPAPKQALPGRIHFSGYDNDRPGNLVYRFDVKDE 300
Db 241 IGMDDYDVALLEKPKHKKFMKIGVSPAPKQALPGRIHFSGYDNDRPGNLVYRFDVKDE 300

Qy 301 TYDLLYQQCDAQPGASGSGVYVVRWKRFQQQKWERKIIFSGHQWDMNGSPQDFNVAVR 360
Db 301 TYDLLYQQCDAQPGASGSGVYVVRWKRFQQQKWERKIIFSGHQWDMNGSPQDFNVAVR 360

Qy 361 ITPKYAQICWIKGNVLDREG 383
Db 361 ITPKYAQICWIKGNVLDREG 383

RESULT 9
US-09-905-381A-261
; Sequence 261, Application US/09905381A
; Patent No. 6818746
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi

; APPLICANT: Botstein, David
; APPLICANT: Deenoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/905,381A
; CURRENT FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 261
; LENGTH: 383
; TYPE: PRT
; ORGANISM: Homo Sapien
US-09-905-381A-261

Query Match 100.0%; Score 2080; DB 4; Length 383;
Best Local Similarity 100.0%; Pred. No. 5.4e-220;
Matches 383; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MAGIPGLLFLFLLCAVGVSPYSAPWKTWPAYRLPVVLPSTLNLAKEPFGAEAKLE 60
Db 1 MAGIPGLLFLFLLCAVGVSPYSAPWKTWPAYRLPVVLPSTLNLAKEPFGAEAKLE 60
Qy 61 VSSSCGQCHKGTPLTVEAKQVLSYETLYANGSRTEQVGIYIILSSSGDGAQHRDGS 120
Db 61 VSSSCGQCHKGTPLTVEAKQVLSYETLYANGSRTEQVGIYIILSSSGDGAQHRDGS 120
Qy 121 SGKRRKRQIYGVDSRFSIFGKDFLLNYPFSTSVKLSCTGTLVAEKHVLTAACHIDG 180
Db 121 SGKRRKRQIYGVDSRFSIFGKDFLLNYPFSTSVKLSCTGTLVAEKHVLTAACHIDG 180
Qy 181 KTVYVGTQKLRVGLFKPKFDGGRGANDSTSAMPEQMKFQWIRVKTHTVPKGIKGNAND 240
Db 181 KTVYVGTQKLRVGLFKPKFDGGRGANDSTSAMPEQMKFQWIRVKTHTVPKGIKGNAND 240
Qy 241 IGMDYDVALLELKKPKRKFEMKIGVSPAKQLPGRIHFGSGYDNDRPGNLVYRFDVKDE 300
Db 241 IGMDYDVALLELKKPKRKFEMKIGVSPAKQLPGRIHFGSGYDNDRPGNLVYRFDVKDE 300
Qy 301 TYDLLYQQCDAQPGASGSGVYVVMWKRQQQKWERKIIGIFSGHQWYDMNGSPQDFNVAVR 360
Db 301 TYDLLYQQCDAQPGASGSGVYVVMWKRQQQKWERKIIGIFSGHQWYDMNGSPQDFNVAVR 360
Qy 361 ITPLKYAICYWIKNYLDRCRG 383
Db 361 ITPLKYAICYWIKNYLDRCRG 383

RESULT 10

US-09-906-618-261

; Sequence 261, Application US/09906618

; Patent No. 6828146

; GENERAL INFORMATION:

; APPLICANT: Genentech, Inc.

; APPLICANT: Ashkenazi, Avi

; APPLICANT: Botstein, David

; APPLICANT: Deenoyers, Luc

; APPLICANT: Eaton, Dan L.

; APPLICANT: Ferrara, Napoleone

; APPLICANT: Filvaroff, Ellen

; APPLICANT: Fong, Sherman

; APPLICANT: Gao, Wei-Qiang

; APPLICANT: Gerber, Hanspeter

; APPLICANT: Gerritsen, Mary E.

; APPLICANT: Goddard, A.

; APPLICANT: Godowski, Paul J.

; APPLICANT: Grimaldi, Christopher J.

; APPLICANT: Gurney, Austin L.

; APPLICANT: Hillan, Kenneth, J.

; APPLICANT: KJavin, Ivar J.

; APPLICANT: Mather, Jennie P.

; APPLICANT: Pan, James

; APPLICANT: Paoni, Nicholas F.

; APPLICANT: Roy, Margaret Ann

; APPLICANT: Stewart, Timothy A.

; APPLICANT: Tumas, Daniel

; APPLICANT: Williams, P. Mickey

; APPLICANT: Wood, William, I.

; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic

; FILE REFERENCE: 10466-14

; CURRENT APPLICATION NUMBER: US/09/906.618

; CURRENT FILING DATE: 2001-07-16

; PRIOR APPLICATION NUMBER: PCT/US00/04414

; PRIOR FILING DATE: 2000-02-22

; PRIOR APPLICATION NUMBER: US 60/143,048

; PRIOR FILING DATE: 1999-07-07

; PRIOR APPLICATION NUMBER: US 60/145,698

; PRIOR FILING DATE: 1999-07-26

; PRIOR APPLICATION NUMBER: US 60/146,222

; PRIOR FILING DATE: 1999-07-28

; PRIOR APPLICATION NUMBER: PCT/US99/20594

; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 261
; LENGTH: 383
; TYPE: PRT
; ORGANISM: Homo Sapien
US-09-906-618-261

Query Match 100.0%; Score 2080; DB 4; Length 383;
Best Local Similarity 100.0%; Pred. No. 5.4e-220;

Matches 383; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MAGIPGLLFLFLLCAVGVSPYSAPWKTWPAYRLPVVLPSTLNLAKEPFGAEAKLE 60
Db 1 MAGIPGLLFLFLLCAVGVSPYSAPWKTWPAYRLPVVLPSTLNLAKEPFGAEAKLE 60
Qy 61 VSSSCGQCHKGTPLTVEAKQVLSYETLYANGSRTEQVGIYIILSSSGDGAQHRDGS 120
Db 61 VSSSCGQCHKGTPLTVEAKQVLSYETLYANGSRTEQVGIYIILSSSGDGAQHRDGS 120
Qy 121 SGKRRKRQIYGVDSRFSIFGKDFLLNYPFSTSVKLSCTGTLVAEKHVLTAACHIDG 180
Db 121 SGKRRKRQIYGVDSRFSIFGKDFLLNYPFSTSVKLSCTGTLVAEKHVLTAACHIDG 180
Qy 181 KTVYVGTQKLRVGLFKPKFDGGRGANDSTSAMPEQMKFQWIRVKTHTVPKGIKGNAND 240
Db 181 KTVYVGTQKLRVGLFKPKFDGGRGANDSTSAMPEQMKFQWIRVKTHTVPKGIKGNAND 240
Qy 241 IGMDYDVALLELKKPKRKFEMKIGVSPAKQLPGRIHFGSGYDNDRPGNLVYRFDVKDE 300
Db 241 IGMDYDVALLELKKPKRKFEMKIGVSPAKQLPGRIHFGSGYDNDRPGNLVYRFDVKDE 300
Qy 301 TYDLLYQQCDAQPGASGSGVYVVMWKRQQQKWERKIIGIFSGHQWYDMNGSPQDFNVAVR 360
Db 301 TYDLLYQQCDAQPGASGSGVYVVMWKRQQQKWERKIIGIFSGHQWYDMNGSPQDFNVAVR 360
Qy 361 ITPLKYAICYWIKNYLDRCRG 383
Db 361 ITPLKYAICYWIKNYLDRCRG 383

RESULT 11

US-09-072-384-15

; Sequence 15, Application US/09072384

; Patent No. 6153420

; GENERAL INFORMATION:

; APPLICANT: Sheppard, Paul O.

; TITLE OF INVENTION: SERINE PROTEASE POLYPEPTIDES

; AND MATERIALS AND METHODS FOR MAKING THEM

NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: ZymoGenetics, Inc.
STREET: 1201 Eastlake Avenue East
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98102
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/072,384
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Parker, Gary E
REGISTRATION NUMBER: 31,648
REFERENCE/DOCKET NUMBER: 97-16C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-442-6673
TELEFAX: 206-442-6678
TELEX:

INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 392 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
FRAGMENT TYPE: internal
FEATURE:
NAME/KEY: Signal Sequence
LOCATION: 1...19
OTHER INFORMATION:
US-09-072-384-15

Query Match 100.0%; Score 2080; DB 3; Length 392;
Best Local Similarity 100.0%; Pred. No. 5.6e-220;
Matches 383; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 1 MAGIPGLLFLFLLCVAVGVSPYSAPWKTWPAYRLPVVLPSTLNLAKEPFGAEAKLE 60
QY 61 VSSSCGPQCHKGTPPTYEAKQYLSYETLYANGSRRTETQVGIYILSSSGDGAQRDGS 120
DB 61 VSSSCGPQCHKGTPPTYEAKQYLSYETLYANGSRRTETQVGIYILSSSGDGAQRDGS 120
QY 121 SGKSRKRQIYGVDSRFSIFGKDFLLNYPSTSVKLSCTGCTGLVAEKHVLTAACHIDG 180
DB 121 SGKSRKRQIYGVDSRFSIFGKDFLLNYPSTSVKLSCTGCTGLVAEKHVLTAACHIDG 180
QY 181 KTVVGTQKLRVGLFKPKFDGGRGANDSTSAMPEQMKFQWIRVKRTHVPKGIKGNAND 240
DB 181 KTVVGTQKLRVGLFKPKFDGGRGANDSTSAMPEQMKFQWIRVKRTHVPKGIKGNAND 240
QY 241 IGMDDYDYLLELKKPKHKKFMKIGVSPPAKQLPGGRIFHFGSYNDPGLNLYVRFCDVKDE 300
DB 241 IGMDDYDYLLELKKPKHKKFMKIGVSPPAKQLPGGRIFHFGSYNDPGLNLYVRFCDVKDE 300
QY 301 TYDLLYQQCDAQPCAGSGGVYVVMWKQKQKWERKIIIGFSGHQWDMNGSPQDFNVAVR 360
DB 301 TYDLLYQQCDAQPCAGSGGVYVVMWKQKQKWERKIIIGFSGHQWDMNGSPQDFNVAVR 360
QY 361 ITPKVAQICYWIKNYLDREG 383
DB 361 ITPKVAQICYWIKNYLDREG 383

RESULT 12
US-09-072-384-2
Sequence 2, Application US/09072384
Patent No. 6153420
GENERAL INFORMATION:
APPLICANT: Sheppard, Paul O.
TITLE OF INVENTION: SERINE PROTEASE POLYPEPTIDES
AND MATERIALS AND METHODS FOR MAKING THEM
TITLE OF INVENTION: 18
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: ZymoGenetics, Inc.
STREET: 1201 Eastlake Avenue East
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98102
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/072,384
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Parker, Gary E
REGISTRATION NUMBER: 31,648
REFERENCE/DOCKET NUMBER: 97-16C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-442-6673
TELEFAX: 206-442-6678
TELEX:
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 392 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
FRAGMENT TYPE: internal
FEATURE:
NAME/KEY: Signal Sequence
LOCATION: 1...19
OTHER INFORMATION:
US-09-072-384-2

Query Match 98.3%; Score 2044; DB 3; Length 392;
Best Local Similarity 98.4%; Pred. No. 5.1e-216;
Matches 377; Conservative 1; Mismatches 5; Indels 0; Gaps 0;
QY 1 MAGIPGLLFLFLLCVAVGVSPYSAPWKTWPAYRLPVVLPSTLNLAKEPFGAEAKLE 60
DB 1 MAGIPGLLFLFLLCVAVGVSPYSAPWKTWPAYRLPVVLPSTLNLAKEPFGAEAKLE 60
QY 61 VSSSCGPQCHKGTPPTYEAKQYLSYETLYANGSRRTETQVGIYILSSSGDGAQRDGS 120
DB 61 VSSSCGPQCHKGTPPTYEAKQYLSYETLYANGSRRTETQVGIYILSSSGDGAQRDGS 120
QY 121 SGKSRKRQIYGVDSRFSIFGKDFLLNYPSTSVKLSCTGCTGLVAEKHVLTAACHIDG 180
DB 121 SGKSRKRQIYGVDSRFSIFGKDFLLNYPSTSVKLSCTGCTGLVAEKHVLTAACHIDG 180
QY 181 KTVVGTQKLRVGLFKPKFDGGRGANDSTSAMPEQMKFQWIRVKRTHVPKGIKGNAND 240
DB 181 KTVVGTQKLRVGLFKPKFDGGRGANDSTSAMPEQMKFQWIRVKRTHVPKGIKGNAND 240
QY 241 IGMDDYDYLLELKKPKHKKFMKIGVSPPAKQLPGGRIFHFGSYNDPGLNLYVRFCDVKDE 300

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Db 241 IGDYDVALLELKKPKRKKFMKIGVSPAKQLPGRIHFSGYDNDRPNLVYRFDVKDE 300
Qy 301 TYDLLYQCCDAQPGASGGVYVVMWRQOQKWKRIIGIFSGHQWDMNGSPQDFNVAVR 360
Db 301 TYDLLYQCCDAQPGASGGVYVVMWRQOQKWKRIIGIFSGHQWDMNGSPQDFNVAVR 360
Qy 361 ITPKVAQICWIKGNLYDCREG 383
Db 361 ITPKVAQICWIKGNLYDCREG 383

RESULT 13
US-09-551-826D-6
; Sequence 6, Application US/09551826D
; Patent No. 6558939
; GENERAL INFORMATION:
; APPLICANT: No. 6558939regaard-Madsen, Mads
; APPLICANT: Ostergaard, Peter Rahbek
; APPLICANT: Christensen, Claus Bo Voge
; APPLICANT: Lassen, Soren Flenated
; TITLE OF INVENTION: No. 6558939el Poteases And Variants Thereof
; FILE REFERENCE: 5665.200-US
; CURRENT APPLICATION NUMBER: US/09/551,826D
; CURRENT FILING DATE: 2000-04-17
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 6
; LENGTH: 314
; TYPE: PRT
; ORGANISM: Bacillus licheniformis AC116
US-09-551-826D-6

Query Match 9.7%; Score 202.5; DB 4; Length 314;
Best Local Similarity 24.8%; Pred. No. 2e-13;
Matches 77; Conservative 37; Mismatches 137; Indels 59; Gaps 13;

Qy 85 LSYETLYANGSRRTQV-----GIYLSSSGDG-----AQHRDSSGSKSRKRIQYV 132
Db 37 VSSDPSYKPGSTYDPNIKIDNNGAYSKAPEGTGTPGGSVQAKPKESPAAGPPYSPKSVIG 96
Qy 133 YDSRFSIFGKDFLLNVPFSTSVKLTST---GCTGLVAEKHLVLAACHIDH-GKTYVKGQ 188
Db 97 SDRTRVTD---TTAPFYRAIVHISISSIGCTGLIGPKTVATAGHCVDYTSRSPAGTA 153
Qy 189 KLRVGLKPKFKDGGRGANDSTSAMPEQMKFQIRVKRTHVPKGIKGNANDIGMDYDA 248
Db 154 TVSPG-----RNG-----SAYP-----YGSVTSTRYFIPSGWQSGNSN-----YDYA 190
Qy 249 LLELKKPKRKKFMKIGVSPAKQLPGRIHFSGYDNDRPNLVYRFD---VKDETLDLY 306
Db 191 AIELSQPIGNTVGVFGYSYATSSLAGAGVTISGPGDKTTGTQWMSGTTIAVSETYKLQY 250
Qy 307 QCCDAQPGASGGVYVVMWRQOQKWKRII-----GIFSGHQWDMNGSPQDFNVAVRIT 362
Db 251 -AIDTYGGQSGVPYKESSTRTNCSGPCSLAVHTNGVYGG-----SSYNRGTRIT 299
Qy 363 PLKYAQCW 372
Db 300 KEVFDNFTSW 309

RESULT 14
US-09-551-826D-2
; Sequence 2, Application US/09551826D
; Patent No. 6558939
; GENERAL INFORMATION:
; APPLICANT: No. 6558939regaard-Madsen, Mads
; APPLICANT: Ostergaard, Peter Rahbek
; APPLICANT: Christensen, Claus Bo Voge
; APPLICANT: Lassen, Soren Flenated
; TITLE OF INVENTION: No. 6558939el Poteases And Variants Thereof
; FILE REFERENCE: 5665.200-US
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; CURRENT APPLICATION NUMBER: US/09/551,826D
; CURRENT FILING DATE: 2000-04-17
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2
; LENGTH: 316
; TYPE: PRT
; ORGANISM: Bacillus licheniformis
US-09-551-826D-2

Query Match 9.3%; Score 193; DB 4; Length 316;
Best Local Similarity 24.0%; Pred. No. 2.2e-12;
Matches 79; Conservative 43; Mismatches 143; Indels 64; Gaps 15;

Qy 63 SSCGPQCHRGTPU---PTYEAKQYLSYETLYANGSRRTQVGIYLSSSGDGAQHRDVG 119
Db 28 AQAAPSPH---TPVSSDPSY-KAETSVTYDPHIKS-----DQVGLYSKAFGTGKVNETKE 79
Qy 120 SSGKSRKRIQYGYDSRFSIFGKDFLLN-----YPFSTSVKLTST---GCTGLVAEKHV 170
Db 80 KAEKKSAPAKAPY---SIKSVIGSDDRTRVTNTTAYPYRAIVHISISSIGCTGMMIGPKTV 136
Qy 171 LTAACHIHGKT-YVKGTKLVRGLKPKFKDGGRGANDSTSAMPEQMKFQIRVKRTHV 229
Db 137 ATAGHCITYDTSSGSPAGTATVSPG-----RNGTS-----YPYGSVKSTRYFI 178
Qy 230 PKGIWKNANDIGMDYDVALLELKKPKRKKFMKIGVSPAKQLPGGRIHFSGYDNDRPN 289
Db 179 PSGRWSGNTN---YDYGAIELSEPIGNTVGVFGYSYTTSSLVGTTVTITISGYPGDKTAG 233
Qy 290 LVYRFD---VKDETLDLYQCCDAQPGASGGVYVVMWRQOQKWKRII-----GIFSGH 343
Db 234 TQWQHSGPITAISETYKLYAM-DTYGGQSGSPVFEQSSRTNCSGPCSLAVHTNGVYGG- 291
Qy 344 QWDMNGSPQDFNVAVRITPLKYAQCW 372
Db 292 -----SSYNRGTRITKEVFDNLTNW 311

RESULT 15
US-08-090-048-1
; Sequence 1, Application US/08090048
; Patent No. 5523237
; GENERAL INFORMATION:
; APPLICANT: Budtz, Peter
; APPLICANT: Nielsen, Per M.
; TITLE OF INVENTION: PROTEIN PREPARATIONS
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSSEE: No. 5523237o No. 5523237disk of No. 5523237th America, Inc.
; STREET: 405 Lexington Avenue, 62nd Floor
; CITY: New York
; STATE: New York
; COUNTRY: United States of America
; ZIP: 10174-6201
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/090,048
; FILING DATE: 16-JUL-1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DK 199/91
; FILING DATE: 06-FEB-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/DK92/00036
; FILING DATE: 06-FEB-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Agria, Cheryl H.
; REGISTRATION NUMBER: 34,086
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, REFERENCE/DOCKET NUMBER: 3396.214-US
, TELECOMMUNICATION INFORMATION:
, TELEPHONE: 212-867-0123
, TELEFAX: 212-867-0398
, INFORMATION FOR SEQ ID NO: 1:
, SEQUENCE CHARACTERISTICS:
, LENGTH: 222 amino acids
, TYPE: amino acid
, STRANDEDNESS: single
, TOPOLOGY: linear
, MOLECULE TYPE: protein
US-08-090-048-1

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Query Match	8.5%;	Score 177;	DB 1;	Length 222;
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		: : :	: : :	
204	QY	RCANSTSAMPEQMKFQWIRVKRTHV	PKGWIKNANDIGMDYDVALLEKKPKHKFMKI	263
		: : :	: : :	
67	DBB	----RNGTS-----	YPYGSVKSTRYFIPSGWRSGNTN-----YDYGAIETSEPIGNTVGYF	113
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264	QY	GVSPPAKQLPGGRIHSGFYDNDRPNGLN	LVRYFCB--VKDETYDILLYOQCDAAQPGASGSGVY	321
		: : :	: : :	
114	DBB	GYSYTTSSLVGTVTVTISGPGDKTAGTQ	QWHSQFIAISETYKLOYAM-DTYGQSGSGSPVF	172
		: : :	: : :	
322	QY	VRWVKRQQQKWERKII----	GIPSGHQWDMNGSPQDFNVAVRITPLKYAQICYW	372
		: : :	: : :	
173	DB	EQSSRRNTSGGPCSLAVHTNGTVYGG-----	SSYNRGTRITKEVFONLTNW	217

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Job time : 26.9272 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: July 1, 2005, 21:08:25 ; Search time 88.2836 Seconds
(without alignments)
1673.692 Million cell updates/sec

Title: US-09-658-677-18
Perfect score: 2080
Sequence: 1 MAGIPGLLFLPFLCAVGQ.....LKQAICYWIKGNVLDREG 383

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1722976 seqs, 385795295 residues
Total number of hits satisfying chosen parameters: 1722976

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA:*

- 1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
- 2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
- 4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
- 5: /cgn2_6/ptodata/1/pubpaa/PCTUS_NEW_PUB.pep.*
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- 9: /cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep.*
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- 11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep.*
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- 14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
- 15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep.*
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- 18: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
- 19: /cgn2_6/ptodata/1/pubpaa/US11A_PUBCOMB.pep.*
- 20: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep.*
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- 22: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	2080	100.0	383	9	US-09-909-320-261
3	2080	100.0	383	9	US-09-909-088B-261
4	2080	100.0	383	9	US-09-905-291A-261
5	2080	100.0	383	9	US-09-902-853-261
6	2080	100.0	383	9	US-09-907-824-261
7	2080	100.0	383	9	US-09-907-841-261
8	2080	100.0	383	10	US-09-904-011-261
9	2080	100.0	383	10	US-09-903-640-261
10	2080	100.0	383	10	US-09-908-093-261
11	2080	100.0	383	10	US-09-906-742-261

12	2080	100.0	383	10	US-09-906-838-261	Sequence 261, App
13	2080	100.0	383	10	US-09-907-613-261	Sequence 261, App
14	2080	100.0	383	10	US-09-907-942-261	Sequence 261, App
15	2080	100.0	383	10	US-09-904-859-261	Sequence 261, App
16	2080	100.0	383	10	US-09-909-204-261	Sequence 261, App
17	2080	100.0	383	10	US-09-904-820-261	Sequence 261, App
18	2080	100.0	383	10	US-09-904-786-261	Sequence 261, App
19	2080	100.0	383	10	US-09-906-646-261	Sequence 261, App
20	2080	100.0	383	10	US-09-906-700-261	Sequence 261, App
21	2080	100.0	383	10	US-09-903-786-261	Sequence 261, App
22	2080	100.0	383	10	US-09-902-903-261	Sequence 261, App
23	2080	100.0	383	10	US-09-903-749A-261	Sequence 261, App
24	2080	100.0	383	10	US-09-904-119-261	Sequence 261, App
25	2080	100.0	383	10	US-09-904-956-261	Sequence 261, App
26	2080	100.0	383	10	US-09-902-736-261	Sequence 261, App
27	2080	100.0	383	10	US-09-907-794-261	Sequence 261, App
28	2080	100.0	383	10	US-09-903-943-261	Sequence 261, App
29	2080	100.0	383	10	US-09-904-462-261	Sequence 261, App
30	2080	100.0	383	10	US-09-907-925-261	Sequence 261, App
31	2080	100.0	383	10	US-09-903-692-261	Sequence 261, App
32	2080	100.0	383	10	US-09-903-520-261	Sequence 261, App
33	2080	100.0	383	10	US-09-905-056-261	Sequence 261, App
34	2080	100.0	383	10	US-09-984-130-45	Sequence 45, Appl
35	2080	100.0	383	10	US-09-984-130-126	Sequence 126, App
36	2080	100.0	383	10	US-09-909-064-261	Sequence 261, App
37	2080	100.0	383	10	US-09-904-553-261	Sequence 261, App
38	2080	100.0	383	10	US-09-905-381-261	Sequence 261, App
39	2080	100.0	383	10	US-09-904-485-261	Sequence 261, App
40	2080	100.0	383	10	US-09-905-348-261	Sequence 261, App
41	2080	100.0	383	10	US-09-905-088-261	Sequence 261, App
42	2080	100.0	383	10	US-09-907-575-261	Sequence 261, App
43	2080	100.0	383	10	US-09-905-075-261	Sequence 261, App
44	2080	100.0	383	10	US-09-902-759-261	Sequence 261, App
45	2080	100.0	383	10	US-09-902-634-261	Sequence 261, App

ALIGNMENTS

RESULT 1
US-09-765-205-12
; Sequence 12, Application US/09765205
; Patent No. US20020034800A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Li
; TITLE OF INVENTION: BONE MARROW SECRETED PROTEINS AND POLYNUCLEOTIDES
; FILE REFERENCE: 1458.004/200130.449
; CURRENT APPLICATION NUMBER: US/09/765,205
; CURRENT FILING DATE: 2001-01-17
; PRIOR APPLICATION NUMBER: US/09/212,440
; PRIOR FILING DATE: 1998-12-16
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 12
; LENGTH: 383
; TYPE: PRT
; ORGANISM: human
; US-09-765-205-12

Query Match	100.0%;	Score	2080;	DB	9;	Length	383;
Best Local Similarity	100.0%;	Pred. No.	1.2e-194;				
Matches	383;	Conservative	0;	Mismatches	0;	Indels	0;
						Gaps	0;
Qy	1	MAGIPGLLFLLPFLCAVGQVSPYSAPWKPTWPAYRLPVVLPQSTLNLA	KPFGAEAKLE	60			
Db	1	MAGIPGLLFLLPFLCAVGQVSPYSAPWKPTWPAYRLPVVLPQSTLNLA	KPFGAEAKLE	60			
Qy	61	VSSSCGPQCHKGTPLPTYEAKQVLSYETLYANGSRTETQVGIVILSSG	BGAQHRDGS	120			
Db	61	VSSSCGPQCHKGTPLPTYEAKQVLSYETLYANGSRTETQVGIVILSSG	BGAQHRDGS	120			
Qy	121	SGKSRKRQIYGVDSRPSIFGKDFLLNYPFSTSVKLSITGCTGLVAEKH	VLTAARCIHDG	180			

Db 121 SGKRRKRQIYGVDSRFSIFGKDFLLNYPFSTSVKLSGTCTGLVAEKHVLTAACHIDG 180
Qy 181 KTVYVGTQKLRVGLFKPKFDGGRGANDSTSAMPEQMKFQWIRVKTHTHPKGIKGNAND 240
Db 181 KTVYVGTQKLRVGLFKPKFDGGRGANDSTSAMPEQMKFQWIRVKTHTHPKGIKGNAND 240
Qy 241 IGMDYDVALLELKKPHKRKFMKIGVSPAKQLPGGRIFHFGSYDNDPRGNLVYRFDVKDE 300
Db 241 IGMDYDVALLELKKPHKRKFMKIGVSPAKQLPGGRIFHFGSYDNDPRGNLVYRFDVKDE 300
Qy 301 TYDLLYQCCDAQPCASGSGVYVMMKROQOKWERKIIIGIFSGHGWVDMNGSPQDENVAVR 360
Db 301 TYDLLYQCCDAQPCASGSGVYVMMKROQOKWERKIIIGIFSGHGWVDMNGSPQDENVAVR 360
Qy 361 ITPLKYAQICYWIKGNVLDREG 383
Db 361 ITPLKYAQICYWIKGNVLDREG 383

RESULT 2
US-09-909-320-261
; Sequence 261, Application US/09909320
; Patent No. US20020132240A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A. Paul J.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/909,320
; CURRENT FILING DATE: 2002-01-04
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214

; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 261
; LENGTH: 383
; TYPE: PRT
; ORGANISM: Homo Sapien
US-09-909-320-261

Query Match 100.0%; Score 2080; DB 9; Length 383;
Best Local Similarity 100.0%; Pred. No. 1.2e-194; Indels 0; Gaps 0;
Matches 383; Conservative 0; Mismatches 0;

Qy 1 MAGIPGLLELFLLCAGVQVSPYSAPWKPTWPAYRLPVVLPQSTLNLAQPDFAEAKLE 60
Db 1 MAGIPGLLELFLLCAGVQVSPYSAPWKPTWPAYRLPVVLPQSTLNLAQPDFAEAKLE 60
Qy 61 VSSSCGPOCHKGTPPTYBEAKQYLSYETLYANGSRTETQVGIYILSSSGDGAQHRDGS 120
Db 61 VSSSCGPOCHKGTPPTYBEAKQYLSYETLYANGSRTETQVGIYILSSSGDGAQHRDGS 120
Qy 121 SGKRRKRQIYGVDSRFSIFGKDFLLNYPFSTSVKLSGTCTGLVAEKHVLTAACHIDG 180
Db 121 SGKRRKRQIYGVDSRFSIFGKDFLLNYPFSTSVKLSGTCTGLVAEKHVLTAACHIDG 180
Qy 181 KTVYVGTQKLRVGLFKPKFDGGRGANDSTSAMPEQMKFQWIRVKTHTHPKGIKGNAND 240
Db 181 KTVYVGTQKLRVGLFKPKFDGGRGANDSTSAMPEQMKFQWIRVKTHTHPKGIKGNAND 240
Qy 241 IGMDYDVALLELKKPHKRKFMKIGVSPAKQLPGGRIFHFGSYDNDPRGNLVYRFDVKDE 300
Db 241 IGMDYDVALLELKKPHKRKFMKIGVSPAKQLPGGRIFHFGSYDNDPRGNLVYRFDVKDE 300
Qy 301 TYDLLYQCCDAQPCASGSGVYVMMKROQOKWERKIIIGIFSGHGWVDMNGSPQDENVAVR 360
Db 301 TYDLLYQCCDAQPCASGSGVYVMMKROQOKWERKIIIGIFSGHGWVDMNGSPQDENVAVR 360
Qy 361 ITPLKYAQICYWIKGNVLDREG 383
Db 361 ITPLKYAQICYWIKGNVLDREG 383

RESULT 3
US-09-909-088B-261
; Sequence 261, Application US/09909088B
; Patent No. US20020146709A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A. Paul J.
; APPLICANT: Godowski, Paul J.


```
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kijavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/909/088B
; CURRENT FILING DATE: 2001-07-18
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 261
; LENGTH: 383
; TYPE: PRT
; ORGANISM: Homo Sapien
; US-09-909-088B-261

Query Match 100.0%; Score 2080; DB 9; Length 383;
Best Local Similarity 100.0%; Pred. No. 1.2e-194;
Matches 383; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MAGIPGLLFLFLLCAGVQSPYAPWKTWPAYRLPVVLPQSTLNLAKPFGAEAKLE 60
Db 1 MAGIPGLLFLFLLCAGVQSPYAPWKTWPAYRLPVVLPQSTLNLAKPFGAEAKLE 60
Qy 61 VSSSCGPOCHKCTPLPYEAKQYLSVETLYANGSRTEQVGIYILSSGSGAQHRDGS 120
Db 61 VSSSCGPOCHKCTPLPYEAKQYLSVETLYANGSRTEQVGIYILSSGSGAQHRDGS 120
Qy 121 SGKSRKRQIYGVDSRFSIEGDKFLNYPFSTSVKLSGTGTLVAKKHLVLTAAHCIDHG 180
Db 121 SGKSRKRQIYGVDSRFSIEGDKFLNYPFSTSVKLSGTGTLVAKKHLVLTAAHCIDHG 180
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Qy 181 KTYVKGTKLRVGLPKPKKQGGGRANDSTSAMPEQMKFQWIRKTRTHVPKGMKGNAND 240
Db 181 KTYVKGTKLRVGLPKPKKQGGGRANDSTSAMPEQMKFQWIRKTRTHVPKGMKGNAND 240
Qy 241 IGMDDYDYLLELKKPHKRFKMGKIGVSPPAKQLPGGRHFGSYDNDREGLVYRFGCDVKDE 300
Db 241 IGMDDYDYLLELKKPHKRFKMGKIGVSPPAKQLPGGRHFGSYDNDREGLVYRFGCDVKDE 300
Qy 301 TYDLYQQCDQAQPGASGSGVYVVMWKRQKQKWKRIIGIFSGHQMVMNGSPQDFNVAVR 360
Db 301 TYDLYQQCDQAQPGASGSGVYVVMWKRQKQKWKRIIGIFSGHQMVMNGSPQDFNVAVR 360
Qy 361 ITPKVAQICYWKIGNYLDREG 383
Db 361 ITPKVAQICYWKIGNYLDREG 383

RESULT 4
US-09-905-291A-261
; Sequence 261, Application US/09905291A
; Patent No. US20020160374A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kijavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/905,291A
; CURRENT FILING DATE: 2001-07-12
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
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; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 261
; LENGTH: 383
; TYPE: PRT
; ORGANISM: Homo Sapien
; US-09-905-291A-261

Query Match 100.0%; Score 2080; DB 9; Length 383;
Best Local Similarity 100.0%; Pred No. 1.2e-194;
Matches 383; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MAGIPGLLFLFLLCAGGVSPYSAPWKPTWPAYRLPVVLPQSTLNLAKEPFGAEAKLE 60
Db 1 MAGIPGLLFLFLLCAGGVSPYSAPWKPTWPAYRLPVVLPQSTLNLAKEPFGAEAKLE 60

Qy 61 VSSSCGPOCHKGTPLPTYEAKQYLSYETLYANGSRTEQVGIYILSSGDAQHRDGS 120
Db 61 VSSSCGPOCHKGTPLPTYEAKQYLSYETLYANGSRTEQVGIYILSSGDAQHRDGS 120

Qy 121 SGKSRKRQIYGVDSRFSIFGKDFLLNYPFSTSVKLSCTGTLVAEKHVLTAACHIDG 180
Db 121 SGKSRKRQIYGVDSRFSIFGKDFLLNYPFSTSVKLSCTGTLVAEKHVLTAACHIDG 180

Qy 181 KTVYKGTQKLRVGLFKPKFKDGRGANDSTSAMPEQMKFQIRVKRTHVPKGIKNAND 240
Db 181 KTVYKGTQKLRVGLFKPKFKDGRGANDSTSAMPEQMKFQIRVKRTHVPKGIKNAND 240

Qy 241 IGMDDYALLELKKPKHKKEMKIGVSPKAKOLPGGRHIFSGYDNDPRGNLVYFCVDKDE 300
Db 241 IGMDDYALLELKKPKHKKEMKIGVSPKAKOLPGGRHIFSGYDNDPRGNLVYFCVDKDE 300

Qy 301 TYDLLYQCCDAQPGAGSGGVYVWVKRQOKWERKIIIGIFSGHQWDMNGSPQDFNVAVR 360
Db 301 TYDLLYQCCDAQPGAGSGGVYVWVKRQOKWERKIIIGIFSGHQWDMNGSPQDFNVAVR 360

Qy 361 ITPKVAQICYKGNLYDCREG 383
Db 361 ITPKVAQICYKGNLYDCREG 383

RESULT 5

US-09-902-853-261
; Sequence 261, Application US/09902853
; Publication No. US20020192659A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerlitsen, Mary E.
; APPLICANT: Goddard A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.

; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/902,853
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: US/09/665,350
; PRIOR FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 261
; LENGTH: 383
; TYPE: PRT
; ORGANISM: Homo Sapien
; US-09-902-853-261

Query Match 100.0%; Score 2080; DB 9; Length 383;
Best Local Similarity 100.0%; Pred No. 1.2e-194;
Matches 383; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MAGIPGLLFLFLLCAGGVSPYSAPWKPTWPAYRLPVVLPQSTLNLAKEPFGAEAKLE 60
Db 1 MAGIPGLLFLFLLCAGGVSPYSAPWKPTWPAYRLPVVLPQSTLNLAKEPFGAEAKLE 60

Qy 61 VSSSCGPOCHKGTPLPTYEAKQYLSYETLYANGSRTEQVGIYILSSGDAQHRDGS 120
Db 61 VSSSCGPOCHKGTPLPTYEAKQYLSYETLYANGSRTEQVGIYILSSGDAQHRDGS 120

Qy 121 SGKSRKRQIYGVDSRFSIFGKDFLLNYPFSTSVKLSCTGTLVAEKHVLTAACHIDG 180
Db 121 SGKSRKRQIYGVDSRFSIFGKDFLLNYPFSTSVKLSCTGTLVAEKHVLTAACHIDG 180

Qy	181	KTYVKG	TQKLRVGLFKPKFKKQGGRGANDST	SAMPQMKFQWIRVRKTRHVPKGIKGNAND	244
Db	181	KTYVKG	TQKLRVGLFKPKFKKQGGRGANDST	SAMPQMKFQWIRVRKTRHVPKGIKGNAND	240
Qy	241	IGMDV	DYALLELKPKPKFKFKKIGVSPPAKQLPGGRIHFHSGYDNDRPGNLVVRFCDDVKDE	300	
Db	241	IGMDV	DYALLELKPKPKFKFKKIGVSPPAKQLPGGRIHFHSGYDNDRPGNLVVRFCDDVKDE	300	
Qy	301	TYDLLY	QQCDAQPGASGSGVYVVMWKROQQKWKERKIIGIFSGHQWYDNGSGPQDFNVAVR	360	
Db	301	TYDLLY	QQCDAQPGASGSGVYVVMWKROQQKWKERKIIGIFSGHQWYDNGSGPQDFNVAVR	360	
Qy	361	ITPLKYA	QICYWIKNYLDCREG	383	
Db	361	ITPLKYA	QICYWIKNYLDCREG	383	
RESULT 6					
US-09-907-824-261					
; Sequence 261, Application US/09907824					
; Publication No. US20020197671A1					
; GENERAL INFORMATION:					
; APPLICANT: Genentech, Inc.					
; APPLICANT: Ashkenazi, Avi					
; APPLICANT: Botstein, David					
; APPLICANT: Desnoyers, Luc					
; APPLICANT: Eaton, Dan L.					
; APPLICANT: Ferrara, Napoleone					
; APPLICANT: Filvaroff, Ellen					
; APPLICANT: Fong, Sherman					
; APPLICANT: Gao, Wei-Qiang					
; APPLICANT: Gerber, Hanspeter					
; APPLICANT: Gertsitsen, Mary E.					
; APPLICANT: Goddard, A.					
; APPLICANT: Godowski, Paul J.					
; APPLICANT: Grimaldi, Christopher J.					
; APPLICANT: Gurney, Austin L.					
; APPLICANT: Hillan, Kenneth, J.					
; APPLICANT: Kljavin, Ivar J.					
; APPLICANT: Mather, Jennie P.					
; APPLICANT: Pan, James					
; APPLICANT: Paoni, Nicholas F.					
; APPLICANT: Roy, Margaret Ann					
; APPLICANT: Stewart, Timothy A.					
; APPLICANT: Tumas, Daniel					
; APPLICANT: Williams, P. Mickey					
; APPLICANT: Wood, William, I.					
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic					
; FILE REFERENCE: 10466-14					
; CURRENT APPLICATION NUMBER: US/09/907,824					
; CURRENT FILING DATE: 2001-07-17					
; PRIOR APPLICATION NUMBER: 09/665,350					
; PRIOR FILING DATE: 2000-09-18					
; PRIOR APPLICATION NUMBER: PCT/US00/04414					
; PRIOR FILING DATE: 2000-02-22					
; PRIOR APPLICATION NUMBER: US 60/143,048					
; PRIOR FILING DATE: 1999-07-07					
; PRIOR APPLICATION NUMBER: US 60/145,698					
; PRIOR FILING DATE: 1999-07-26					
; PRIOR APPLICATION NUMBER: US 60/146,222					
; PRIOR FILING DATE: 1999-07-28					
; PRIOR APPLICATION NUMBER: PCT/US99/20594					
; PRIOR FILING DATE: 1999-09-08					
; PRIOR APPLICATION NUMBER: PCT/US99/20944					
; PRIOR FILING DATE: 1999-09-13					
; PRIOR APPLICATION NUMBER: PCT/US99/21090					
; PRIOR FILING DATE: 1999-09-15					
; PRIOR APPLICATION NUMBER: PCT/US99/21547					
; PRIOR FILING DATE: 1999-09-15					
; PRIOR APPLICATION NUMBER: PCT/US99/23089					
; PRIOR FILING DATE: 1999-10-05					
; PRIOR APPLICATION NUMBER: PCT/US99/28214					

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; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/907,841
; CURRENT FILING DATE: 2001-11-20
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 261
; LENGTH: 383
; TYPE: PRT
; ORGANISM: Homo Sapien
; US-09-907-841-261

Query Match          100.0%; Score 2080; DB 9; Length 383;
Best Local Similarity 100.0%; Pred. No. 1.2e-194;
Matches 383; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MAGIPGLLFLFLCAVGQVSPYSAPWKPPTWPAIRLPVVLPOSTLNLAQPDGAEAKLE 60
    |||||
Db 1 MAGIPGLLFLFLCAVGQVSPYSAPWKPPTWPAIRLPVVLPOSTLNLAQPDGAEAKLE 60
    |||||

Qy 61 VSSSCGPQCHGKPTLPYERAKOYLSYETLYANGSRTEQVGIYILSSSGDGAQHRDGS 120
    |||||
Db 61 VSSSCGPQCHGKPTLPYERAKOYLSYETLYANGSRTEQVGIYILSSSGDGAQHRDGS 120
    |||||

Qy 121 SGKRRRKQIYGYDGRFISFGKDFLLNYPFSTSVKLSCTGCTGLVAEKHVLTAACHIDG 180
    |||||
Db 121 SGKRRRKQIYGYDGRFISFGKDFLLNYPFSTSVKLSCTGCTGLVAEKHVLTAACHIDG 180
    |||||

Qy 181 KTVYVGTQKLRVGLFKPKFKDGGGRGANDSTSAMPEQMKFQWIRVVKRTHVPKGIKGNAND 240
    |||||
Db 181 KTVYVGTQKLRVGLFKPKFKDGGGRGANDSTSAMPEQMKFQWIRVVKRTHVPKGIKGNAND 240
    |||||

Qy 241 IGMDDYVALLLEKKPHKPKMKVGVSPAPKQLPGGRIRHFGSGYNDPRGNLVYRFDVKDE 300
    |||||
Db 241 IGMDDYVALLLEKKPHKPKMKVGVSPAPKQLPGGRIRHFGSGYNDPRGNLVYRFDVKDE 300
    |||||

Qy 301 TYDLLYQCDQAQPGASGSGVYVWMKRRQKQKWKRIIGIFSGHQWDMNGSPQDFNVAVR 360
    |||||
Db 301 TYDLLYQCDQAQPGASGSGVYVWMKRRQKQKWKRIIGIFSGHQWDMNGSPQDFNVAVR 360
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Qy 361 ITPLKYAQICYWIKGNYLDCREG 383
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Db 361 ITPLKYAQICYWIKGNYLDCREG 383
    |||||

RESULT 8
US-09-904-011-261
; Sequence 261, Application US/09904011
; Publication No. US20030003530A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/904,011
; CURRENT FILING DATE: 2001-07-11
; PRIOR APPLICATION NUMBER: 09/665,350
; PRIOR FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
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PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US00/00219
PRIOR FILING DATE: 2000-01-05
NUMBER OF SEQ ID NOS: 423
SEQ ID NO 261
LENGTH: 383
TYPE: PRT
ORGANISM: Homo Sapien
US-09-904-011-261

Query Match 100.0%; Score 2080; DB 10; Length 383;
Best Local Similarity 100.0%; Pred. No. 1.2e-194;
Matches 383; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAGIPGLLELLFLLCAVGVSPYSAPWKPPTWYRLPVVLPSTLNLAKEPFGAEAKLE 60
DB 1 MAGIPGLLELLFLLCAVGVSPYSAPWKPPTWYRLPVVLPSTLNLAKEPFGAEAKLE 60

QY 61 VSSSCGPQCHKGTPPTYEAKQYLSYETLYANGSRTEQVGIYILSSSGDGAQHRDGS 120
DB 61 VSSSCGPQCHKGTPPTYEAKQYLSYETLYANGSRTEQVGIYILSSSGDGAQHRDGS 120

QY 121 SGKRRKRQIYGYDSRFSIFGKDFLLNYPSTSVKLSGTCTGLVAEKHVLTAACHIDG 180
DB 121 SGKRRKRQIYGYDSRFSIFGKDFLLNYPSTSVKLSGTCTGLVAEKHVLTAACHIDG 180

QY 181 KTVVGTQKLRVGLFKPKFDDGGRGANDSTSAMPEQMKFQWIRVKTTHVPKGIKGNAND 240
DB 181 KTVVGTQKLRVGLFKPKFDDGGRGANDSTSAMPEQMKFQWIRVKTTHVPKGIKGNAND 240

QY 241 IGMDDYDYLLELKKPKHKKFMKIGVSPPAKQLPGGRIFHSGYDNDPRGNLVYRFDVKDE 300
DB 241 IGMDDYDYLLELKKPKHKKFMKIGVSPPAKQLPGGRIFHSGYDNDPRGNLVYRFDVKDE 300

QY 301 TYDLYQQCDAOPGASGSGVYVMMKRRQOKWERRKIIGIFSGHQWDMNGSPQDFNVAVR 360
DB 301 TYDLYQQCDAOPGASGSGVYVMMKRRQOKWERRKIIGIFSGHQWDMNGSPQDFNVAVR 360

QY 361 ITPKYAQICYWIKGNLYDCREG 383
DB 361 ITPKYAQICYWIKGNLYDCREG 383

RESULT 9
US-09-903-640-261
Sequence 261, Application US/09903640
Publication No. US20030017463A1
GENERAL INFORMATION:
APPLICANT: Genentech, Inc.
APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Geritsen, Mary E.
APPLICANT: Goddard, A.
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, Christopher J.
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth, J.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Mather, Jennie P.
APPLICANT: Pan, James
APPLICANT: Pao, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, I.

TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: 10466-14
CURRENT APPLICATION NUMBER: US/09/903,640
CURRENT FILING DATE: 2001-07-11
PRIOR APPLICATION NUMBER: 09/665,350
PRIOR FILING DATE: 2000-09-18
NUMBER OF SEQ ID NOS: 423
SEQ ID NO 261
LENGTH: 383
TYPE: PRT
ORGANISM: Homo Sapien
US-09-903-640-261

Query Match 100.0%; Score 2080; DB 10; Length 383;
Best Local Similarity 100.0%; Pred. No. 1.2e-194;
Matches 383; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAGIPGLLELLFLLCAVGVSPYSAPWKPPTWYRLPVVLPSTLNLAKEPFGAEAKLE 60
DB 1 MAGIPGLLELLFLLCAVGVSPYSAPWKPPTWYRLPVVLPSTLNLAKEPFGAEAKLE 60

QY 61 VSSSCGPQCHKGTPPTYEAKQYLSYETLYANGSRTEQVGIYILSSSGDGAQHRDGS 120
DB 61 VSSSCGPQCHKGTPPTYEAKQYLSYETLYANGSRTEQVGIYILSSSGDGAQHRDGS 120

QY 121 SGKRRKRQIYGYDSRFSIFGKDFLLNYPSTSVKLSGTCTGLVAEKHVLTAACHIDG 180
DB 121 SGKRRKRQIYGYDSRFSIFGKDFLLNYPSTSVKLSGTCTGLVAEKHVLTAACHIDG 180

QY 181 KTVVGTQKLRVGLFKPKFDDGGRGANDSTSAMPEQMKFQWIRVKTTHVPKGIKGNAND 240
DB 181 KTVVGTQKLRVGLFKPKFDDGGRGANDSTSAMPEQMKFQWIRVKTTHVPKGIKGNAND 240

QY 241 IGMDDYDYLLELKKPKHKKFMKIGVSPPAKQLPGGRIFHSGYDNDPRGNLVYRFDVKDE 300
DB 241 IGMDDYDYLLELKKPKHKKFMKIGVSPPAKQLPGGRIFHSGYDNDPRGNLVYRFDVKDE 300

QY 301 TYDLYQQCDAOPGASGSGVYVMMKRRQOKWERRKIIGIFSGHQWDMNGSPQDFNVAVR 360
DB 301 TYDLYQQCDAOPGASGSGVYVMMKRRQOKWERRKIIGIFSGHQWDMNGSPQDFNVAVR 360

QY 361 ITPKYAQICYWIKGNLYDCREG 383
DB 361 ITPKYAQICYWIKGNLYDCREG 383

RESULT 10
US-09-908-093-261
Sequence 261, Application US/09908093
Publication No. US20030017498A1
GENERAL INFORMATION:
APPLICANT: Genentech, Inc.
APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Geritsen, Mary E.
APPLICANT: Goddard, A.
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, Christopher J.
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth, J.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Mather, Jennie P.
APPLICANT: Pan, James
APPLICANT: Pao, Nicholas F.
APPLICANT: Roy, Margaret Ann

APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: 10466-14
CURRENT APPLICATION NUMBER: US/09/908,093
CURRENT FILING DATE: 2001-07-17
PRIOR APPLICATION NUMBER: 09/665,350
PRIOR FILING DATE: 2000-09-18
PRIOR APPLICATION NUMBER: PCT/US00/04414
PRIOR FILING DATE: 2000-02-22
PRIOR APPLICATION NUMBER: US 60/143,048
PRIOR FILING DATE: 1999-07-07
PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR FILING DATE: 1999-07-26
PRIOR APPLICATION NUMBER: US 60/146,222
PRIOR FILING DATE: 1999-07-28
PRIOR APPLICATION NUMBER: PCT/US99/20594
PRIOR FILING DATE: 1999-09-08
PRIOR APPLICATION NUMBER: PCT/US99/20944
PRIOR FILING DATE: 1999-09-13
PRIOR APPLICATION NUMBER: PCT/US99/21090
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/21547
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/23089
PRIOR FILING DATE: 1999-10-05
PRIOR APPLICATION NUMBER: PCT/US99/28214
PRIOR FILING DATE: 1999-11-29
PRIOR APPLICATION NUMBER: PCT/US99/28313
PRIOR FILING DATE: 1999-11-30
PRIOR APPLICATION NUMBER: PCT/US99/28564
PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/28565
PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/30095
PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: PCT/US99/30911
PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US99/30999
PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US00/00219
PRIOR FILING DATE: 2000-01-05
NUMBER OF SEQ ID NOS: 423
SEQ ID NO 261
LENGTH: 383
TYPE: PRT
ORGANISM: Homo Sapien
US-09-908-093-261

Query Match 100.0%; Score 2080; DB 10; Length 383;
Best Local Similarity 100.0%; Pred. No. 1.2e-194;
Matches 383; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MAGIPGLLFLFLLCAVGVSPYSAPWKPTWPAYRLPVVLPQSTLNLAKEPFGAEAKLE 60
Db 1 MAGIPGLLFLFLLCAVGVSPYSAPWKPTWPAYRLPVVLPQSTLNLAKEPFGAEAKLE 60

Qy 61 VSSSCGQCHKGTPLPYERAKQVLSYETLYANGSRRTQVGIYILSSSGDGAQHRDGS 120
Db 61 VSSSCGQCHKGTPLPYERAKQVLSYETLYANGSRRTQVGIYILSSSGDGAQHRDGS 120

Qy 121 SGKSRKRQIYGVDSRFSIFGKDFLLNYPSTSVKLSGTGCTGLVAEKHVLTAACHIDG 180
Db 121 SGKSRKRQIYGVDSRFSIFGKDFLLNYPSTSVKLSGTGCTGLVAEKHVLTAACHIDG 180

Qy 181 KTVVKGTKLVRGLFKPKFGDGRGANDTSAMPEQMKFQIRVKRTHVPKGIKGNAND 240
Db 181 KTVVKGTKLVRGLFKPKFGDGRGANDTSAMPEQMKFQIRVKRTHVPKGIKGNAND 240

Qy 241 IGMDDYALLELKKPKRKFMKIGVSPPAKQLPGRIHFSGYDNDPRGNLVYRFDVKDE 300

Db 241 IGMDDYALLELKKPKRKFMKIGVSPPAKQLPGRIHFSGYDNDPRGNLVYRFDVKDE 300
Qy 301 TYDLLYQQCDAQPGASGSGVYVMMKROQKWKRIIGIFSGHQWYDMNGSPQDFNVAVR 360
Db 301 TYDLLYQQCDAQPGASGSGVYVMMKROQKWKRIIGIFSGHQWYDMNGSPQDFNVAVR 360
Qy 361 ITPLKYAQICYWIKGNLYDCREG 383
Db 361 ITPLKYAQICYWIKGNLYDCREG 383

RESULT 11
US-09-906-742-261
Sequence 261, Application US/09906742
Publication No. US2003023054A1
GENERAL INFORMATION:
APPLICANT: Genentech, Inc.
APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, A.
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, Christopher J.
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth, J.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Mather, Jennie P.
APPLICANT: Pan, James
APPLICANT: Faoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: 10466-14
CURRENT APPLICATION NUMBER: US/09/906,742
CURRENT FILING DATE: 2001-07-16
PRIOR APPLICATION NUMBER: 09/665,350
PRIOR FILING DATE: 2000-09-18
PRIOR APPLICATION NUMBER: PCT/US00/04414
PRIOR FILING DATE: 2000-02-22
PRIOR APPLICATION NUMBER: US 60/143,048
PRIOR FILING DATE: 1999-07-07
PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR FILING DATE: 1999-07-26
PRIOR APPLICATION NUMBER: US 60/146,222
PRIOR FILING DATE: 1999-07-28
PRIOR APPLICATION NUMBER: PCT/US99/20594
PRIOR FILING DATE: 1999-09-08
PRIOR APPLICATION NUMBER: PCT/US99/20944
PRIOR FILING DATE: 1999-09-13
PRIOR APPLICATION NUMBER: PCT/US99/21090
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/21547
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/23089
PRIOR FILING DATE: 1999-10-05
PRIOR APPLICATION NUMBER: PCT/US99/28214
PRIOR FILING DATE: 1999-11-29
PRIOR APPLICATION NUMBER: PCT/US99/28313
PRIOR FILING DATE: 1999-11-30
PRIOR APPLICATION NUMBER: PCT/US99/28564
PRIOR FILING DATE: 1999-12-02

PRIOR APPLICATION NUMBER: PCT/US99/28565
PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/30095
PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: PCT/US99/30911
PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US99/30999
PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US00/00219
PRIOR FILING DATE: 2000-01-05
NUMBER OF SEQ ID NOS: 423
SEQ ID NO 261
LENGTH: 383
TYPE: PRT
ORGANISM: Homo Sapien
US-09-906-742-261

Query Match 100.0%; Score 2080; DB 10; Length 383;
Best Local Similarity 100.0%; Pred. No. 1.2e-194;
Matches 383; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAGIPGLLFLFLLCAVGVSPYSAPWKPTWPAYRLPVVLPSTLNLAKEPFGAEAKLE 60
DB 1 MAGIPGLLFLFLLCAVGVSPYSAPWKPTWPAYRLPVVLPSTLNLAKEPFGAEAKLE 60
QY 61 VSSSCGPOCHKGTPPTYEEAKQYLSYETLYANGSRTEQVGIYIILSSGDAQHRDGS 120
DB 61 VSSSCGPOCHKGTPPTYEEAKQYLSYETLYANGSRTEQVGIYIILSSGDAQHRDGS 120
QY 121 SGKSRKRQIYGYDSRFSIFGKDFLLNYPSTSVKLSGTCTGLVAEKHVLTAACHIDG 180
DB 121 SGKSRKRQIYGYDSRFSIFGKDFLLNYPSTSVKLSGTCTGLVAEKHVLTAACHIDG 180
QY 181 KTVYVGTQKLRVGLFKPKFQKGGANDSTSAMPEQMKFQWIRVGTHTVFKGWIKNAND 240
DB 181 KTVYVGTQKLRVGLFKPKFQKGGANDSTSAMPEQMKFQWIRVGTHTVFKGWIKNAND 240
QY 241 IGMNDYALLEKPKHKEKMKIGVSPPAKOLPGGRHFSGYNDPRGNLVYFCVQKDE 300
DB 241 IGMNDYALLEKPKHKEKMKIGVSPPAKOLPGGRHFSGYNDPRGNLVYFCVQKDE 300
QY 301 TYDLLYQCCDAOPGASGGVYVWVRKQKQKWKRIIGIFSGHQWDMNGSPQDFNVAVR 360
DB 301 TYDLLYQCCDAOPGASGGVYVWVRKQKQKWKRIIGIFSGHQWDMNGSPQDFNVAVR 360
QY 361 ITPKVAQICYWKGNLYDCREG 383
DB 361 ITPKVAQICYWKGNLYDCREG 383

RESULT 12
US-09-906-838-261
Sequence 261, Application US/09906838
Publication No. US20030027143A1
GENERAL INFORMATION:
APPLICANT: Genentech, Inc.
APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, A.
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, Christopher J.
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth, J.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Mather, Jennie P.

APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: 10466-14
CURRENT APPLICATION NUMBER: US/09/906,838
CURRENT FILING DATE: 2001-07-16
PRIOR APPLICATION NUMBER: 09/665,350
PRIOR FILING DATE: 2000-09-18
PRIOR APPLICATION NUMBER: PCT/US00/04414
PRIOR FILING DATE: 2000-02-22
PRIOR APPLICATION NUMBER: US 60/143,048
PRIOR FILING DATE: 1999-07-07
PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR FILING DATE: 1999-07-26
PRIOR APPLICATION NUMBER: US 60/146,222
PRIOR FILING DATE: 1999-07-28
PRIOR APPLICATION NUMBER: PCT/US99/20594
PRIOR FILING DATE: 1999-09-08
PRIOR APPLICATION NUMBER: PCT/US99/20944
PRIOR FILING DATE: 1999-09-13
PRIOR APPLICATION NUMBER: PCT/US99/21090
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/21547
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/23089
PRIOR FILING DATE: 1999-10-05
PRIOR APPLICATION NUMBER: PCT/US99/28214
PRIOR FILING DATE: 1999-11-29
PRIOR APPLICATION NUMBER: PCT/US99/28313
PRIOR FILING DATE: 1999-11-30
PRIOR APPLICATION NUMBER: PCT/US99/28564
PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/28565
PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/30095
PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: PCT/US99/30911
PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US99/30999
PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US00/00219
PRIOR FILING DATE: 2000-01-05
NUMBER OF SEQ ID NOS: 423
SEQ ID NO 261
LENGTH: 383
TYPE: PRT
ORGANISM: Homo Sapien
US-09-906-838-261

Query Match 100.0%; Score 2080; DB 10; Length 383;
Best Local Similarity 100.0%; Pred. No. 1.2e-194;
Matches 383; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAGIPGLLFLFLLCAVGVSPYSAPWKPTWPAYRLPVVLPSTLNLAKEPFGAEAKLE 60
DB 1 MAGIPGLLFLFLLCAVGVSPYSAPWKPTWPAYRLPVVLPSTLNLAKEPFGAEAKLE 60
QY 61 VSSSCGPOCHKGTPPTYEEAKQYLSYETLYANGSRTEQVGIYIILSSGDAQHRDGS 120
DB 61 VSSSCGPOCHKGTPPTYEEAKQYLSYETLYANGSRTEQVGIYIILSSGDAQHRDGS 120
QY 121 SGKSRKRQIYGYDSRFSIFGKDFLLNYPSTSVKLSGTCTGLVAEKHVLTAACHIDG 180
DB 121 SGKSRKRQIYGYDSRFSIFGKDFLLNYPSTSVKLSGTCTGLVAEKHVLTAACHIDG 180
QY 181 KTVYVGTQKLRVGLFKPKFQKGGANDSTSAMPEQMKFQWIRVGTHTVFKGWIKNAND 240
DB 181 KTVYVGTQKLRVGLFKPKFQKGGANDSTSAMPEQMKFQWIRVGTHTVFKGWIKNAND 240

Db 181 KTVVGTQKLRVGLPKPKFDGGRGANDSTSAMPEQMKQWIRVKRTHVPKGIKGNAND 240
QY 241 IGMDYDVALLELKPKHKKFPMKIGVSPPAKQLPGGRHFSGYDNDPRGNLVYRFDVKDE 300
Db 241 IGMDYDVALLELKPKHKKFPMKIGVSPPAKQLPGGRHFSGYDNDPRGNLVYRFDVKDE 300
QY 301 TYDLLYQOCDAQPGASGSGVYVVMKROQOKWERKIIGIFSGHQWDMNGSPQDFNVAVR 360
Db 301 TYDLLYQOCDAQPGASGSGVYVVMKROQOKWERKIIGIFSGHQWDMNGSPQDFNVAVR 360
QY 361 ITPLKYAQICYWIKGNLYDCREG 383
Db 361 ITPLKYAQICYWIKGNLYDCREG 383

RESULT 13

US-09-907-613-261
; Sequence 261, Application US/09907613
; Publication No. US20030027145A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/907,613
; CURRENT FILING DATE: 2001-07-17
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564

; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 261
; LENGTH: 383
; TYPE: PRT
; ORGANISM: Homo Sapien
US-09-907-613-261

Query Match 100.0%; Score 2080; DB 10; Length 383;
Best Local Similarity 100.0%; Pred. No. 1.2e-194;
Matches 383; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAGIPGLLFLFLCAVGVSPYSAPWKPTWPAYRLPVVLPVLTNLAQKPDFAEAKLE 60
Db 1 MAGIPGLLFLFLCAVGVSPYSAPWKPTWPAYRLPVVLPVLTNLAQKPDFAEAKLE 60

QY 61 VSSSCGPQCHKGTPLPTVEEAKQYLSYETLYANGSRTEQVGIYIILSSGDSGAQHRDGS 120
Db 61 VSSSCGPQCHKGTPLPTVEEAKQYLSYETLYANGSRTEQVGIYIILSSGDSGAQHRDGS 120

QY 121 SGKSRKRQIYGDSRFSIFGKDFLLNYPFSTSVKLSCTGCTGLVAEKHVLTAACHIDG 180
Db 121 SGKSRKRQIYGDSRFSIFGKDFLLNYPFSTSVKLSCTGCTGLVAEKHVLTAACHIDG 180

QY 181 KTVVGTQKLRVGLPKPKFDGGRGANDSTSAMPEQMKQWIRVKRTHVPKGIKGNAND 240
Db 181 KTVVGTQKLRVGLPKPKFDGGRGANDSTSAMPEQMKQWIRVKRTHVPKGIKGNAND 240

QY 241 IGMDYDVALLELKPKHKKFPMKIGVSPPAKQLPGGRHFSGYDNDPRGNLVYRFDVKDE 300
Db 241 IGMDYDVALLELKPKHKKFPMKIGVSPPAKQLPGGRHFSGYDNDPRGNLVYRFDVKDE 300

QY 301 TYDLLYQOCDAQPGASGSGVYVVMKROQOKWERKIIGIFSGHQWDMNGSPQDFNVAVR 360
Db 301 TYDLLYQOCDAQPGASGSGVYVVMKROQOKWERKIIGIFSGHQWDMNGSPQDFNVAVR 360

QY 361 ITPLKYAQICYWIKGNLYDCREG 383
Db 361 ITPLKYAQICYWIKGNLYDCREG 383

RESULT 14

US-09-907-942-261
; Sequence 261, Application US/09907942
; Publication No. US20030027146A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.


```

; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/907,942
; CURRENT FILING DATE: 2002-01-22
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 261
; LENGTH: 383
; TYPE: PRT
; ORGANISM: Homo Sapien
; US-09-907-942-261

Query Match 100.0%; Score 2080; DB 10; Length 383;
Best Local Similarity 100.0%; Pred. No. 1.2e-194;
Matches 383; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAGIPGLLFLFLLCVAGQVSPYSAPWKPWPAYRLPVVLPQSTLNLAKEPFGAEAKLE 60
DB 1 MAGIPGLLFLFLLCVAGQVSPYSAPWKPWPAYRLPVVLPQSTLNLAKEPFGAEAKLE 60

QY 61 VSSSCGQCHGTPLPTPYEAKQVLSYETLYANGSRTEQVGIYILSSSGDGAQHRDSGS 120
DB 61 VSSSCGQCHGTPLPTPYEAKQVLSYETLYANGSRTEQVGIYILSSSGDGAQHRDSGS 120

QY 121 SGKSRKQIYGVDSRFISFGKDFLLNYPSTSVKLTGCTGLVAEKHVLTAACHIDG 180
DB 121 SGKSRKQIYGVDSRFISFGKDFLLNYPSTSVKLTGCTGLVAEKHVLTAACHIDG 180

QY 181 KTVVKGQKLRVGLFKPKFKDGGGRANDSTSAMPEQMKFQWIRVKRTHVPKGIKNAND 240
DB 181 KTVVKGQKLRVGLFKPKFKDGGGRANDSTSAMPEQMKFQWIRVKRTHVPKGIKNAND 240

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QY 241 IGMDDYALLELKKPKRKMKGVSPPAKQLPGGRIFHSFGYDNDPRGNLVYFCDVKDE 300
DB 241 IGMDDYALLELKKPKRKMKGVSPPAKQLPGGRIFHSFGYDNDPRGNLVYFCDVKDE 300

QY 301 TYDLLYQCCDAQPGASGSGVYVVMWKRQOQKWERKIIGIFSGHQWDMNGSPQDFNVAVR 360
DB 301 TYDLLYQCCDAQPGASGSGVYVVMWKRQOQKWERKIIGIFSGHQWDMNGSPQDFNVAVR 360

QY 361 ITPKYAQICYWIKGNLYDCREG 383
DB 361 ITPKYAQICYWIKGNLYDCREG 383

RESULT 15
US-09-904-859-261
; Sequence 261, Application US/09904859
; Publication No. US200300306060A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/904,859
; CURRENT FILING DATE: 2001-07-12
; PRIOR APPLICATION NUMBER: 09/665,350
; PRIOR FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30

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; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 261
; LENGTH: 383
; TYPE: PRT
; ORGANISM: Homo Sapien
US-09-904-859-261

Query Match      100.0%; Score 2080; DB 10; Length 383;
Best Local Similarity 100.0%; Pred. No. 1.2e-194;
Matches 383; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1  MAGIPGLLFLFLCAVGVSPYSAPKPTWPAYRLPVVLPOSTLNLAKEPFGAEAKLE 60
Db      1  MAGIPGLLFLFLCAVGVSPYSAPKPTWPAYRLPVVLPOSTLNLAKEPFGAEAKLE 60

Qy     61  VSSSCGPGCHKGTPLPYEEAKQVLSYETLYANGSRRTETQVGIYILSSSGDGAQHRDSGS 120
Db     61  VSSSCGPGCHKGTPLPYEEAKQVLSYETLYANGSRRTETQVGIYILSSSGDGAQHRDSGS 120

Qy    121  SGKSRKRQIYGYDSRFSIFGKDFLLNYPFSTSVKLTGCTGTTLVAEKHVLTAACHIDG 180
Db    121  SGKSRKRQIYGYDSRFSIFGKDFLLNYPFSTSVKLTGCTGTTLVAEKHVLTAACHIDG 180

Qy    181  KTYVKGTKLRLVGLKPKFKDGGGANDSTSAMPEQMKFQWIRVKTHTVPEKGIKGNAND 240
Db    181  KTYVKGTKLRLVGLKPKFKDGGGANDSTSAMPEQMKFQWIRVKTHTVPEKGIKGNAND 240

Qy    241  IGMDDYDYLLELKKPHKRPKMGVSPPAKQLPGRIHFSGYDNDRPGNLVYRFCVVKDE 300
Db    241  IGMDDYDYLLELKKPHKRPKMGVSPPAKQLPGRIHFSGYDNDRPGNLVYRFCVVKDE 300

Qy    301  TYDLLYQCCDAQPGASGSGVYVRMWKQQQKWERKIIGIFSGHQWVDMNGSPQDFNVAVR 360
Db    301  TYDLLYQCCDAQPGASGSGVYVRMWKQQQKWERKIIGIFSGHQWVDMNGSPQDFNVAVR 360

Qy    361  ITPLKYAQICYWIKGNVLDREG 383
Db    361  ITPLKYAQICYWIKGNVLDREG 383
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Search completed: July 1, 2005, 21:32:18
Job time : 89.2836 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: July 1, 2005, 20:54:23 ; Search time 20.3479 Seconds
(without alignments)
1811.048 Million cell updates/sec

Title: US-09-658-677-18

Perfect score: 2080

Sequence: 1 MAGIPGLFLFLFLCAVGQ.....LKQAICYWIKGNLYLDCREG 383

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR 79:*

1: PIR1:*

2: PIR2:*

3: PIR3:*

4: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	194	9.3	316	2 A45134	endopeptidase (EC
2	135.5	6.5	313	2 A35122	metalloproteinase
3	131	6.3	218	2 E97915	choline binding pr
4	120.5	5.8	482	1 EXRT	coagulation factor
5	119	5.7	269	2 A26823	pancreatic elastas
6	117	5.6	522	2 T29767	hypothetical prote
7	115.5	5.6	289	2 B26823	pancreatic elastas
8	115.5	5.6	271	2 A25528	pancreatic elastas
9	115	5.5	258	4 S70439	pancreatic elastas
10	115	5.5	267	4 A56615	probable pancreati
11	114.5	5.5	238	1 TRW5Y	trypsin-like prote
12	114.5	5.5	285	2 C95045	choline binding pr
13	114	5.5	246	1 DBHU	complement factor
14	113	5.4	266	1 ELPG	pancreatic elastas
15	113	5.4	266	1 ELRT1	pancreatic elastas
16	112.5	5.4	259	1 TRSMG	trypsin (EC 3.4.21
17	112.5	5.4	273	2 E85765	hypothetical prote
18	112.5	5.4	273	2 H64915	Putative protease
19	111.5	5.4	488	1 EXHU	coagulation factor
20	111	5.3	761	2 JC5759	brain-specific ser
21	110	5.3	269	2 C26823	pancreatic elastas
22	110	5.3	492	1 EXBO	coagulation factor
23	110	5.3	1582	2 T15308	hypothetical prote
24	109.5	5.3	405	2 T35117	probable secreted
25	109	5.2	278	2 A20282	probable peptidas
26	108	5.2	583	2 A29154	complement factor
27	108	5.2	786	1 A47547	serine proteinase
28	108	5.2	1047	2 A55617	masquerade precurs
29	107.5	5.2	236	2 A28566	T-cell suppressor

30	107.5	5.2	686	1 A59271	Ra-reactive factor
31	105	5.0	274	2 S40004	trypsin-related pr
32	103.5	5.0	271	1 ELRT2	pancreatic elastas
33	103.5	5.0	416	1 KFO	coagulation factor
34	102.5	4.9	1238	2 T34929	hypothetical prote
35	100	4.8	272	2 JC4170	trypsin-like prote
36	98.5	4.7	267	2 S40006	trypsin (EC 3.4.21
37	98	4.7	548	2 D82175	probable trypsin v
38	98	4.7	624	2 T02289	membrane-bound arg
39	98	4.7	855	2 JC7731	probable polygalac
40	97.5	4.7	409	2 T35118	probable secreted
41	97.5	4.7	452	1 A30351	coagulation factor
42	97.5	4.7	747	2 I51579	complement factor
43	97	4.7	1019	2 A38738	coagulation factor
44	96.5	4.6	259	2 S68424	allergen Der f III
45	96.5	4.6	275	2 I46712	factor IX - rabbit

ALIGNMENTS

RESULT 1

A45134

endopeptidase (EC 3.4.-.-), glutamate-specific - Bacillus licheniformis

C:Species: Bacillus licheniformis

C>Date: 10-Jun-1993 #sequence_revision 18-Nov-1994 #text_change 16-Aug-2004

C/Accession: A45134, S23078

R;Kakudo, S.; Kikuchi, N.; Kitadokoro, K.; Fujiwara, T.; Nakamura, E.; Okamoto, H.; Shin,

J. Biol. Chem. 267, 23782-23788, 1992

A;Title: Purification, characterization, cloning, and expression of a glutamic acid-speci

A;Reference number: A45134; MUID:93054737; PMID:1429718

A;Accession: A45134

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-316 <KAK>

A;Cross-references: UNIPROT:P80057; GB:D10060; NID:g216263; PIDN:BAA00949.1; PID:d100141

A;Experimental source: ATCC 14580

A;Note: sequence extracted from NCBI backbone (NCBIN:118784, NCBIP:118785)

R;Svendsen, I.; Breddam, K.

Eur. J. Biochem. 204, 165-171, 1992

A;Title: Isolation and amino acid sequence of a glutamic acid specific endopeptidase from

A;Reference number: S23078; MUID:92155199; PMID:1346764

A;Accession: S23078

A;Status: preliminary

A;Molecule type: protein

A;Residues: 95-316 <SVE>

C;Superfamily: Glutamyl endopeptidase, V8 type

C;Keywords: hydrolase

Query Match 9.3%; Score 194; DB 2; Length 316;

Best Local Similarity 24.0%; Pred. No. 1.7e-08;

Matches 79; Conservative 43; Mismatches 143; Indels 64; Gaps 15;

QY 63 SSGPQCHKGTPL---PTVEAKQVLSYETLVANGSRRTETQVGIYILSSSGCAQHRDSG 119

Db 28 AQAPSPH--TPVSSDPSTY-KAETSVTDP-----NIKSDQYGLYSKAFGTGKVNETKE 79

QY 120 SSGKSRKRQIYGYDSRSPFPGKDFLLN-----YPFSTSVKLST---GCTGLTVAEKHV 170

Db 80 KAEKSPAKAPY---SIKSVIGSDDRTRVNTTAYPYRAIVHSSISGCTGWMIGPKTV 136

QY 171 LTAHCIHDKGT-YVKGTKLRVGLFKPKFGKGRANDSTAMPQMKFQWTRVKRTHV 229

Db 137 ATAGHCIDYTSSGSFAGTATVSPG-----RNGTS-----YPYGSVKSTRFYI 178

QY 230 PKGWTKGNANDIGMDYDVALLELKPKHRKFKMGIVSPPAKQLPGGRIHFSGYDNDRPGN 289

Db 179 PGWRSNGTN-----YDYGAIELSEPIGNVTGVFGYSYTTSSLVGTVTISGPGDKTAG 233

QY 290 LVYRFCD---VKDETLLYQQCDAQPFASGSGGVYVRMKRQQQKWERKII---GIFSGH 343

Db 234 TQWHSGLPTAISTYKLYQAM-DTYGQSGSPVFEQSSSRSTNCSCPSLAVHTNGVYGG- 291

QY 344 QWVDMNGSPQDFNVAVRITPLKVAQICYW 372
Db 292 -----SSYNRGTRITKEVFDNLTNW 311

RESULT 2
A35122
metalloproteinase (EC 3.4.21.6) mpr precursor, extracellular - Bacillus subtilis
C:Species: Bacillus subtilis
C:Date: 27-Jul-1990 #sequence_revision 27-Jul-1990 #text_change 16-Aug-2004
C:Accession: A35122; I40010; A69660
R:Sloma, A.; Rudolph, C.F.; Rufo Jr., G.A.; Sullivan, B.J.; Theriault, K.A.; Ally, D.; F
J. Bacteriol. 172, 1024-1029, 1990
A:Title: Gene encoding a novel extracellular metalloprotease in Bacillus subtilis.
A:Reference number: A35122; MUID:90130256; PMID:2105291
A:Accession: A35122
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-313 <SLO>
A:Cross-references: UNIPROT:P39790; GB:L10505; NID:G143209; PIDN:AAA22604.1; PID:G143210
R:Smith, H.; de Jong, A.; Bron, S.; Venema, G.
Gene 70, 351-361, 1988
A:Title: Characterization of signal-sequence-coding regions selected from the Bacillus s
A:Reference number: I39994; MUID:99108019; PMID:3145906
A:Accession: I40010
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-60, 65, 'L', '67', 'S', '69', 'AOK' <RES>
A:Cross-references: GB:M2916; NID:G143701; PIDN:AAA22832.1; PID:G143702
R:Kunst, P.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berte
C.; Bron, S.; Brouillet, S.; Bruchi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Ch
A.; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.
Nature 390, 249-256, 1997
A:Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Gall
iech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F.
Koertter, P.; Koningsstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois,
A:Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maueel
M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelle
Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanlon,
A:Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Seron
akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiyama
T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, K
A:Authors: Yoshikawa, H.F.; Zumbstein, E.; Yoshikawa, H.; Danchin, A.
A:Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.
A:Reference number: A69580; MUID:98044033; PMID:9384377
A:Accession: A69560
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-313 <KUN>
A:Cross-references: GB:Z99105; GB:AL009126; NID:G2632457; PIDN:CABI2018.1; PID:G1182176;
A:Experimental source: strain 168
C:Genetics:
A:Gene: mpr
C:Superfamily: Glutamyl endopeptidase, V8 type
C:Keywords: hydrolase

Query Match 6.5%; Score 135.5; DB 2; Length 313;
Best Local Similarity 22.2%; Pred. No. 0.0013;
Matches 77; Conservative 38; Mismatches 121; Indels 111; Gaps 17;

QY 72 GTPLPYVEAKQYLVETLYANGSRTEQVIGYILSSGD--GAQHRDSSGSKSRKQ 129
Db 29 GVPKAAENPQTSVNTGKEADATKNQT-----SKADQVAPYEGTGKTSK----- 75

QY 130 IYGVDSRF-----STFGKD-----FLNYPSTSVKLSL-----GCTGTL 164
Db 76 LYGGQTELEKNIOTLPQSSIIGDTERISSTTSFPYRATVQUSIKYPNSTSYGCTGFL 135

QY 165 VAERKHLVTAARCIH-----DGKTYVKGQKLRVGLKPKFKDGGRGAND 208
Db 136 VNPNTVVTAGHCYVSQDHGWASTTAAPGRNGSSYPGY----- 175

QY 209 STSAMPEQMKFQIRVKRTHVPKWKIGN---ANDIGMDYDYLLELKKPKHKKFKMKIGV 265

Db 176 -SGTFYSVK-GWTBSKDTNYDYGAIKLNGSPGNTVGM-YGRTNNSSP-----VGL 225
QY 266 SPPAKQLPGGRIHFSGYDNDPRGNLVYRFDVKDEYDLLYQQCAQPAQSGSGVYVRMW 325
Db 226 SSSVTGFPDCDKTFGIMWSDTKPIR-----SAETYKLTYYTDTYGCQSGSPVY---- 272

QY 326 KRQOQKWERKIIFPSGHQWDMNGSPQDFNVAVRITPLKVAQICYW 372
Db 273 -RNYSDTGQTATAIHT-----NGG-SSYNLGTRVNDVFNNIQYW 310

RESULT 3
E97915
choline binding protein G, truncation [imported] - Streptococcus pneumoniae (strain R6)
C:Species: Streptococcus pneumoniae
C:Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 09-Jul-2004
C:Accession: E97915
R:Hoskins, J.A.; Alborn Jr., W.; Arnold, J.; Blaszcak, L.; Burgett, S.; DeHoff, B.S.; E
e, R.; LeBlanc, D.J.; Lee, L.N.; Lefkowitz, E.J.; Lu, J.; Matsushima, P.; McAhren, S.; M
Y, P.; Sun, P.M.; Winkler, M.E.
J. Bacteriol. 183, 5709-5717, 2001
A:Authors: Yang, Y.; Young-Bellido, M.; Zhao, G.; Zook, C.; Baltz, R.H.; Jaskunas, S.R.;
A:Title: Genome of the Bacterium Streptococcus pneumoniae Strain R6.
A:Reference number: A97872; MUID:21429245; PMID:11544234
A:Accession: E97915
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-218 <KUR>
A:Cross-references: UNIPROT:Q8DR41; GB:AE007317; PIDN:AAK99153.1; PID:G15457907; GSPDB:G
C:Genetics:
A:Gene: cbpG-truncation

Query Match 6.3%; Score 131; DB 2; Length 218;
Best Local Similarity 24.2%; Pred. No. 0.0019;
Matches 59; Conservative 30; Mismatches 87; Indels 68; Gaps 10;

QY 143 DFLNYPSTSVKLSGTCG-----TLVAEKHVLTAACHIDHGKTYVKGTOK 189
Db 5 DNTLQVPYSTSAWLSKYVGADGMNVEGRGSANFIKONVLITAAH-----NYR----- 54

QY 190 LRVGLKPKFKDGGRGAND---STSMPEQMKFQIRVKRTHVPKWKIGNANDIGMDYD 246
Db 55 -----HDYGEADIIYVLPVAVSPSQELFKIKVKEVRYLKEFRNLNSKD-AREYD 103

QY 247 YALLEKPKHKKFKMKIGVSPPAKQLPGGRIHFSGYDNDPRGNLVYR-----CDVKOE 300
Db 104 LALLILEKPIGAKLTGLGLPTSQKNLTGITVITGYPS-----YNFKIHQWYTDKKQV 156

QY 301 TYD---LLYQOQDAQPGASGGVYVRMKRQOQKWERKIIFPSGHQWDMNGSPQDFNV 357
Db 157 LSDDGMFLDYQVDTLEGSSGSTVY-----DASHRVVGVHT-----LGDGANQINS 201

QY 358 AVRI 361
Db 202 AVKL 205

RESULT 4
EXRT
cosulation factor Xa (EC 3.4.21.6) precursor - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 31-Jan-1995 #sequence_revision 07-Feb-1997 #text_change 09-Jul-2004
C:Accession: S49075; J04670; PS0191; PS0190; I62745
R:Stanton, C.; Ross, P.; Hutson, S.; Wallin, R.
Thromb. Res. 80, 63-73, 1995
A:Title: Evidence for competition between vitamin K-dependent clotting factors for intrac
A:Reference number: A58498; MUID:96093366; PMID:8578539
A:Accession: S49075
A:Molecule type: mRNA
A:Residues: 1-482 <STAL>
A:Cross-references: UNIPROT:Q63207; EMBL:X79807; NID:G506600; PIDN:CAA56202.1; PID:G50660
A:Note: submitted to the EMBL Data Library, June 1994

R;Note: neither the complete nucleic acid sequence nor the complete translation are shown
R;Stanton, C.; Ross, R.P.; Huteon, S.; Wallin, R.
Gene 169, 269-273, 1996
A;Title: Processing and expression of rat and human clotting factor-X-encoding cDNAs.
A;Reference number: JC4670; MUID:96194815; PMID:8647460
A;Accession: JC4670
A;Molecule type: mRNA
A;Residues: 1-482 <STA2>
A;Cross-references: EMBL:X79807; NID:g506600; PIDN:CAA56202.1; PID:g506601
A;Experimental source: Cos-1 cell
R;Enyoji, K.; Miyazaki, K.; Kato, H.
J. Biochem. 109, 890-898, 1991
A;Title: Characterization of rat factors X and Xa: demonstration of factor Xa in rat plasma
A;Reference number: PS0190; MUID:92041742; PMID:1718949
A;Accession: PS0191
A;Molecule type: protein
A;Residues: 41-58, 'X', 60-65 <ENJ1>
A;Accession: PS0190
A;Molecule type: protein
R;Murakawa, M.; Okamura, T.; Kamura, T.; Kuroiwa, M.; Harada, M.; Niho, Y.
Eur. J. Haematol. 52, 162-168, 1994
A;Title: Analysis of the partial nucleotide sequences and deduced primary structures of factor Xa
A;Reference number: I46196; MUID:94222160; PMID:8168596
A;Accession: I62745
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 295-383, 'G', 385-455 <MUR>
A;Cross-references: GB:D21215; NID:g415309; PIDN:BA04756.1; PID:g455396
C;Function:
A;Description: catalyzes the proteolytic activation of prothrombin to thrombin in the presence of calcium ions
A;Pathway: blood coagulation
C;Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homology
C;Keywords: beta-hydroxyaspartic acid; blood coagulation; calcium binding; carboxyglutamate
F;1-23/Domain: signal sequence #status predicted <SIG>
F;24-40/Domain: propeptide #status predicted <PRO>
F;25-84/Domain: Gla domain homology <GLA>
F;41-179/Product: coagulation factor X light chain #status predicted <LCH>
F;90-121/Domain: EGF homology <EG1>
F;129-164/Domain: EGF homology <EG2>
F;183-482/Product: coagulation factor X heavy chain #status predicted <HCH>
F;183-231/Domain: activation peptide #status predicted <APT>
F;232-482/Product: coagulation factor Xa heavy chain #status predicted <ACT>
F;232-460/Domain: trypsin homology <TRY>
F;46,47,54,56,59,60,65,66,69,72,79/Modified site: gamma-carboxyglutamic acid (Glu) #status predicted <MOD>
F;57-62,90-101,95-110,112-121,129-140,136-149,151-164,172-340,238-243,259-275,308-402,411-421/Modified site: erythro-beta-hydroxyaspartic acid (Asp) #status predicted <MOD>
F;103/Modified site: carboxy-beta-hydroxyaspartic acid (Asp) #status predicted <MOD>
F;187/Binding site: carboxy-beta-hydroxyaspartic acid (Asp) #status experimental
F;208/Binding site: carboxy-beta-hydroxyaspartic acid (Asp) #status predicted
F;218/Binding site: carboxy-beta-hydroxyaspartic acid (Asp) #status predicted
F;231-232/Cleavage site: Arg-Ile (coagulation factor IXa, coagulation factor VIIa) #status predicted
F;274,320,417/Active site: His, Asp, Ser #status predicted

Query Match 5.8%; Score 120.5; DB 1; Length 482;
Best Local Similarity 32.3%; Pred. No. 0.038;
Matches 31; Conservative 17; Mismatches 23; Indels 25; Gaps 4;
A;Introns: 36/2; 138/3; 234/2; 311/1; 331/1; 421/1; 470/2

QY 160 CTCTLVAEKHVLTAACHIDHDKTYVKGTKLVGFLKPKFKDGGGANDSTAMPQMKF 219
DB 259 CGGTILNEFVILTAACHLQAKRF-----KVRVGLNTEQEDGGMVHE-VDMIKHNKF 312

QY 220 QWTRVVRKTHVPKWKGNANDIGMDYDYLLELKKP 255
DB 313 Q-----RDTY-----DFDIAMLRKLT 329

RESULT 5
A26823
pancreatic elastase II (EC 3.4.21.71) precursor - pig
N;Alternate names: pancratopeptidase E
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 16-Aug-1988 #sequence_revision 16-Aug-1988 #text_change 09-Jul-2004
C;Accession: A26823

R;Kawashima, I.; Tani, T.; Shimoda, K.; Takiguchi, Y.
DNA 6, 163-172, 1987
A;Title: Characterization of pancreatic elastase II cDNAs: two elastase II mRNAs are expressed from a single gene
A;Reference number: A90958; MUID:87217962; PMID:3646943
A;Accession: A26823
A;Molecule type: mRNA
A;Residues: 1-269 <KAW>
A;Cross-references: UNIPROT:P08419; GB:M16651; NID:g164441; PIDN:AAA31027.1; PID:g164442
C;Superfamily: trypsin; trypsin homology
C;Keywords: hydrolyase; serine proteinase
F;1-16/Domain: signal sequence #status predicted <SIG>
F;17-28/Domain: propeptide #status predicted <PRO>
F;29-269/Product: elastase II #status predicted <MAT>
F;29-262/Domain: trypsin homology <TRY>
F;73,121,216/Active site: His, Asp, Ser #status predicted

Query Match 5.7%; Score 119; DB 2; Length 269;
Best Local Similarity 27.5%; Pred. No. 0.024;
Matches 60; Conservative 28; Mismatches 64; Indels 66; Gaps 14;

QY 128 RQIYGYDSRFSIFGKDFLLNYPSTSVKL-STG-----CTGTLVAEKHVLTAACHIDGK 181
DB 28 RVVGGEDARPN-----SWPMQVSLQYDSSGQWRHTCGTTLVDOSWVLTAAHCISSSR 79

QY 182 TY--VKGTKLVGFLKPKFKDGGGANDSTAMPQMKFQWIRVVRKTHVPKWKGNAN 239
DB 80 TYRVVLGRHSL-----STNEPGLA-----VKVSKLVVHQDW---NSN 114

QY 240 DIGMDYDYLLELKKP-HRKRPMKIGVSPPAKQ-LFG-----GRIHFGSYDND--R 286
DB 115 QLSNGNDIALKLKASPVSLTDKIQCLPAAGTILPNVYVYVTGWRGLQTNGASPDILQ 174

QY 287 PGMVTRFCDVDETDLLYQQCDAPGASGSGVYRM 324
DB 175 QGOLL-----VVD-----YATC-SKPGWGWSTVKTNM 200

RESULT 6
T29767
Hypothetical protein ZC581.6 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T29767
R;Waterston, B.; Gattung, S.; Le, T.T.
submitted to the EMBL Data Library, May 1997
A;Description: The sequence of C. elegans cosmid ZC581.
A;Reference number: Z20682
A;Accession: T29767
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-522 <MAT>
A;Cross-references: UNIPROT:O01771; EMBL:AF003134; PIDN:AAB54144.1; GSPDB:GN00019; CESP:1
A;Experimental source: strain Bristol N2; clone ZC581
C;Genetics:
A;Gene: CESP:ZC581.6
A;Map position: 1
A;Introns: 36/2; 138/3; 234/2; 311/1; 331/1; 421/1; 470/2

Query Match 5.6%; Score 117; DB 2; Length 522;
Best Local Similarity 20.4%; Pred. No. 0.082;
Matches 95; Conservative 56; Mismatches 153; Indels 162; Gaps 21;

QY 29 KPTWPAIRLPVVLPOSTNLAKPFGAEAKLEVSS---CGPOCHKGTPLPTVEAKQ-- 83
DB 26 KPSNKASSAPSLRKKSSSNPNKGTARSVSKVPKSAIPASPTVQKEVPPVEIKKKEK 85

QY 84 -----YLSYETLYANGSRTEQVGIYILSSSDGQAHRDSSGSGKRRKRIQYVDSRF 137
DB 86 PENQKKEAEKKL-----DRTQDDGKEKAEASALGVVVIKEDKAPAKMDGVEDFGPCECF 141

QY 138 SIFGKD-----FLNYPFSTV-----KLSTGCCTGTLVAEK 168
DB 142 PFLKILEMILWLRIPFSAKYNVGRDASQSEAPWSVFTYLYSKDQSQATTCGTIVSPR 201

A;Status: preliminary; not compared with conceptual translation
A;Molecule type: DNA
A;Residues: 1-258 <KAW>
A;Note: it is not known whether the gene is expressed
F;19-251/Domain: trypsin homology <TRY>

Query Match 5.5%; Score 115; DB 4; Length 258;
Best Local Similarity 26.9%; Pred. No. 0.05;
Matches 35; Conservative 23; Mismatches 38; Indels 34; Gaps 6;
QY 147 NYPFSTSVKLGSTG-----CTGTLVAEKHLVLTAAHCIDHDKTY--VKGTKLRVGFLLPK 198
DB 29 SWPSQISLQVRSGGSWYHTCGTLIRQNWVMTAAHCVDYQKTRVWAGDHNL-----80
QY 199 FKDGRCANDSTAMPQKFWIRVTRVTPKGVKGNANDIGMDYDYLLEL-KKPHK 257
DB 81 -----SONDGT-----QYVSQKIVVHPYV-----NSDNVAAGYDIALRLAQSRTL 123
QY 258 RKFMKIGVSP 267
DB 124 NSYVQLGVLP 133

RESULT 10
A56615
probable pancreatic elastase (EC 3.4.21.36) pseudogene - human
N;Alternate names: pancreatic elastase I homolog; pancreatic elastase I allele HEL1-16,
C;Species: Homo sapiens (man)
C;Date: 11-Aug-1995 #sequence_revision 17-Aug-1995 #text_change 14-Aug-1998
C;Accession: A56615; S70440
R;Kawashima, I.; Tani, T.; Mita-Honjo, K.; Shimoda-Takano, K.; Ohmine, T.; Furukawa, H.;
DNA Seq. 2, 303-312, 1992
A;Title: Genomic organization of the human homologue of the rat pancreatic elastase I ge
A;Reference number: A56615; MUID:92338395; PMID:1633328
A;Accession: A56615
A;Molecule type: DNA
A;Residues: 1-267 <KAW>
A;Cross-references: EMBL:X62259; NID:931246; EMBL:X62258; GB:S40923; NID:931247; EMBL:X6
5; GB:S40856; NID:931251; EMBL:X62256; GB:S40857; NID:931252; EMBL:X62257; GB:S40859; NI
C;Note: sequence extracted from NCBI backbone (NCBIN:109315, NCBIN:109317, NCBIN:109319,
C;Comment: This apparently silent human homolog of pancreatic elastase I is a single-co
unctional protein in some other tissue.
C;Genetics:
A;Gene: GDB:ELAI
A;Map position: 12
C;Keywords: hydrolase; pseudogene; serine proteinase

Query Match 5.5%; Score 115; DB 4; Length 267;
Best Local Similarity 26.9%; Pred. No. 0.052;
Matches 35; Conservative 23; Mismatches 38; Indels 34; Gaps 6;
QY 147 NYPFSTSVKLGSTG-----CTGTLVAEKHLVLTAAHCIDHDKTY--VKGTKLRVGFLLPK 198
DB 38 SWPSQISLQVRSGGSWYHTCGTLIRQNWVMTAAHCVDYQKTRVWAGDHNL-----89
QY 199 FKDGRCANDSTAMPQKFWIRVTRVTPKGVKGNANDIGMDYDYLLEL-KKPHK 257
DB 90 -----SONDGT-----QYVSQKIVVHPYV-----NSDNVAAGYDIALRLAQSRTL 132
QY 258 RKFMKIGVSP 267
DB 133 NSYVQLGVLP 142

RESULT 11
TRW5Y
trypsin-like proteinase (EC 3.4.21.-) SGI precursor - yellow fever mosquito (fragment)
C;Species: Aedes aegypti (yellow fever mosquito)
C;Date: 31-Dec-1992 #sequence_revision 31-Dec-1992 #text_change 09-Jul-2004
C;Accession: S19891
R;Kalhok, S.; Tabak, L.M.; Prosser, D.E.; Downe, A.E.R.; White, B.N.
submitted to the EMBL Data Library, February 1992
A;Description: Isolation, sequencing and characterization of 2 cDNA clones coding for tr

A;Reference number: S19890
A;Accession: S19891
A;Molecule type: mRNA
A;Residues: 1-238 <KAL>

A;Cross-references: UNIPROT:P29787; EMBL:X64363; NID:95563; PIDN:CAA45715.1; PID:95564
C;Superfamily: trypsin; trypsin homology
C;Keywords: hydrolase; insect midgut; protein digestion; serine proteinase
F;1-11/Domain: signal sequence and propeptide (fragment) #status predicted <SIG>
F;12-238/Product: trypsin-like proteinase SGI #status predicted <MAT>
F;12-232/Domain: trypsin homology <TRY>
F;38-54,162-178,189-213/Distulfide bonds: #status predicted
F;53,97,193/Active site: His, Asp, Ser #status predicted

Query Match 5.5%; Score 114.5; DB 1; Length 238;
Best Local Similarity 29.4%; Pred. No. 0.05; DB 1; Length 238;
Matches 42; Conservative 22; Mismatches 44; Indels 35; Gaps 7;
QY 149 PFSTSTSVKLGSTGCTTLVAEKHLVLTAAHCIDHDKTYVKGTKLRVGFLLPKFKDGGRG 205
DB 24 PFQVSLSGVSGSHFPGCGSLLSERVWVTAGCAASGGTNL-----QVRIG--SSQHASGG--75
QY 206 ANDSTAMPQKFWIRVTRVTPKGVKGNANDIGMDYDYLLELKKPHKFKFKWIG 264
DB 76 -----OLIKVKVNRHPK-----YDEVTTDYDPALLELEETVTFSDSCAP 115
QY 265 VSPPAKOLP---CGRIHFSGYDN 284
DB 116 VKLPQKQDTPVNEGTCLQVSGWN 138

RESULT 12
C95045
choline binding protein G [imported] - Streptococcus pneumoniae (strain TIGR4)
C;Species: Streptococcus pneumoniae
C;Date: 03-Aug-2001 #sequence_revision 03-Aug-2001 #text_change 09-Jul-2004
C;Accession: C95045
R;Tetzelin, H.; Nelson, K.E.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson, S.; Heide
nson, J.D.; Hickey, E.K.; Holt, I.E.
Science 293, 498-506, 2001
A;Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morrison,
A;Title: Complete Genome Sequence of a virulent isolate of Streptococcus pneumoniae.
A;Reference number: A95000; MUID:21357209; PMID:11463916
A;Accession: C95045
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-285 <KUR>
A;Cross-references: UNIPROT:Q97SH5; GB:AE005672; PIDN:AAK74556.1; PID:gl4971860; GSPDB:G
A;Experimental source: strain TIGR4
C;Genetics:
A;Gene: SP0390

Query Match 5.5%; Score 114.5; DB 2; Length 285;
Best Local Similarity 23.4%; Pred. No. 0.062;
Matches 54; Conservative 31; Mismatches 91; Indels 55; Gaps 9;
QY 161 TGTVAEKHLVLTAAHCIDHDKTYVKGTKLRVGFLLPKFKDGGRGAND---STSAMPEQM 217
DB 20 SANFIKDNVLTAAH-----NYR-----HDYKGEADDIVLPAVSPSQE 59
QY 218 KQWIRVTRVTPKGVKGNANDIGMDYDYLLELKKPHKFKFKWIGVSPPAKOLPGRI 277
DB 60 PFGIKVKEVRYLKKEFRNLNSKD-AREYDLALLILEEPTGAKLGLTGLTPTSQNLGTITV 118
QY 278 HFSGYDNDPGLVRYF-----CDVKDETYD---LLYQCDAPGASGSGVYVVRWKQ 328
DB 119 TTIGYPS-----YFKIHWMTDKKQVLSDDGMFLDVQVDTLESGSGSTVY-----164
QY 329 QQKWERKIIFSGHQWDMNGSPQDFNVAVTRPLTKYAQICWYIKGNVLD 379
DB 165 --DASHRVVGVT-----LGDGANQINSVAVKLNRNLPFIYSVLKGYSLE 207

RESULT 13

DBHU
complement factor D (EC 3.4.21.46) precursor [validated] - human (fragment)
N;Alternate names: adipsin; C3 convertase activator
C;Species: Homo sapiens (man)
C;Date: 28-Aug-1985 #sequence_revision 31-Dec-1992 #text_change 09-Jul-2004
C;Accession: A40197; A00936; A60571; S66645
R;White, R.T.; Damm, D.; Hancock, N.; Rosen, B.S.; Lowell, B.B.; Usher, P.; Flier, J.S.;
J. Biol. Chem. 267, 9210-9213, 1992
A;Title: Human adipsin is identical to complement factor D and is expressed at high level
A;Reference number: A40197; MUID:92250520; PMID:1374388
A;Accession: A40197
A;Molecule type: mRNA
A;Residues: 1-246 <WHI>
A;Cross-references: UNIPROT:P00746; GB:M84526
R;Niemann, M.A.; Bhowm, A.S.; Bennett, J.C.; Volanakis, J.E.
Biochemistry 23, 2482-2486, 1984
A;Title: Amino acid sequence of human D of the alternative complement pathway.
A;Reference number: A00936; MUID:85000441; PMID:6383466
A;Accession: A00936
A;Molecule type: protein
A;Residues: 19-44, 'G', 46-51, 'O', 53-75, 'TH', 78, 'P', 80-83, 'XXXITIR', 90-172, 86-91, 185-235, '
A;Note: a few residues were assigned from the previously published sequence of Reid et al.
R;Miyata, T.; Oda, O.; Inagi, R.; Sugiyama, S.; Miyama, A.; Maeda, K.; Nakashima, I.; Ya
Mol. Immunol. 27, 637-644, 1990
A;Title: Molecular and functional identification and purification of complement component
A;Reference number: A60571; MUID:90370044; PMID:2395435
A;Accession: A60571
A;Molecule type: protein
A;Residues: 19-20, 'XX', 23-27, 'XX', 30-31, 'XX', 34, 'X', 36-40 <MIY>
R;Baik, N.; Holtkamp, U.; Hoerl, W.H.; Tschesche, H.
FEBS Lett. 371, 300-302, 1995
A;Title: Inhibition of degradation of human polymorphonuclear leukocytes by complement
A;Reference number: S66645; MUID:96013156; PMID:7556615
A;Accession: S66645
A;Status: preliminary
A;Molecule type: protein
A;Residues: 19-44, 'C', 46-48 <BAL>
C;Comment: Factor D cleaves factor B when the latter is complexed with factor C3b, activ
C;Genetics:
A;Gene: GDB:DF
A;Cross-references: GDB:132645; OMIM:134350
A;Map position: Xpter-Xqter
C;Superfamily: trypsin; trypsin homology
C;Keywords: complement alternate pathway; hydrolase; plasma; serine proteinase
F;1-18/Domain: signal sequence #status predicted <SIG>
F;19-246/Product: complement factor D (fragment) #status experimental <MAT>
F;19-241/Domain: trypsin homology <TRY>
F;44-60,141-207,172-188,197-222/Disulfide bonds: #status predicted
F;59,105,201/Active site: His, Asp, Ser #status predicted

Query Match 5.58; Score 114; DB 1; Length 246;
Best Local Similarity 28.4%; Pred. No. 0.057;
Matches 44; Conservative 20; Mismatches 43; Indels 48; Gaps 9;

QY 149 PFSTSVKLSGTG--CTGTLVAEKHLVTAACHIH---DQKTYVKGTLKRVGLKPKFDGG 203
DB 31 PYMASVQLNGAHLCAVLVAERVLSAAHCLDAADGKQVLT----- 72
QY 204 RGANDSTSAMPEQMKFQWIRVKRTHVPKGNANDIGMDYDYALLELKKPKRPMKI 263
DB 73 LGAHSLSQEPFKRLVDLRA---VP---HPDSQPDTHDHLILQLSE-----KA 117
QY 264 GVSPAPKQLPGGRTHFGSGYDND-RPGNLVYRFCDV 297
DB 118 TLGPAVRPLPQQRV-----DRDVAPGFL-----CDV 143

RESULT 14

ELPG
pancreatic elastase (EC 3.4.21.36) I precursor - pig
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 24-Apr-1984 #sequence_revision 30-Sep-1990 #text_change 09-Jul-2004

C;Accession: JS0013; A26777; A10061; A00959
R;Shitamu, Y.; Yoshida, H.; Mikayama, T.; Matsuki, S.; Tanaka, J.I.; Ikenaga, H.
J. Biochem. 99, 1707-1712, 1986
A;Title: Isolation and expression in Escherichia coli of a cDNA clone encoding porcine p
A;Reference number: A92005; MUID:86304235; PMID:3528137
A;Accession: JS0013
A;Molecule type: mRNA
A;Residues: 1-266 <SHI>
A;Cross-references: UNIPROT:P00772; GB:X04036; GB:D00070; GB:N00070; NID:g1941; PIDN:CAA;
R;Tani, T.; Kawashima, I.; Furukawa, H.; Ohmine, T.; Takiguchi, Y.
J. Biochem. 101, 591-599, 1987
A;Title: Characterization of a silent gene for human pancreatic elastase I: structure of
A;Reference number: A26777; MUID:87250343; PMID:3648024
A;Accession: A26777
A;Molecule type: mRNA
A;Residues: 1-125, 'G', 127-183, 'L', 185-266 <TAN>
A;Cross-references: GB:D00160; NID:9217683; PIDN:BAA00118.1; PID:g217684
A;Note: the authors translated the codon GGG for residue 58 as Gln, GGC for residue 126
R;Shotton, D.M.; Hartley, B.S.
Biochem. J. 131, 643-675, 1973
A;Title: Evidence for the amino acid sequence of porcine pancreatic elastase.
A;Reference number: A90267; MUID:73229121; PMID:4578945
A;Accession: A10061
A;Molecule type: protein
A;Residues: 27-91, 'N', 93-203, 'N', 205-266 <SHO>
R;Shotton, D.M.; Hartley, B.S.
Nature 225, 811-816, 1970
A;Title: Three-dimensional structure of tosyl-elastase.
A;Reference number: A93160; MUID:70114044; PMID:5415110
A;Contents: annotation; X-ray crystallography, 3.5 angstroms; active site
C;Superfamily: trypsin; trypsin homology
C;Keywords: hydrolase; pancreas; serine proteinase; zymogen
F;1-16/Domain: signal sequence #status predicted <SIG>
F;17-26/Domain: activation peptide #status predicted <APT>
F;27-266/Product: elastase I #status experimental <MAT>
F;27-259/Domain: trypsin homology <TRY>
F;56-72,153-220,184-200,210-240/Disulfide bonds: #status experimental
F;71,119,214/Active site: His, Asp, Ser #status experimental

Query Match 5.4%; Score 113; DB 1; Length 266;
Best Local Similarity 27.3%; Pred. No. 0.076;
Matches 36; Conservative 21; Mismatches 41; Indels 34; Gaps 6;

QY 147 NYPFSTSVKLSGTG-----CTGTLVAEKHLVTAACHIDGKTY--VKGTQKLRVGLKPK 198
DB 37 SNFSQISLQYRSGSSWAHTCGGTLIRQNWMTAAHCVDRLELFRVVVGEHNL----- 88
QY 199 FKDGGERGANDSTSAMPEQMKFQWIRVKRTHVPKGNANDIGMDYDYALLEL-KKPHK 257
DB 89 -----NQNDGTE-----QYVGQKIVVHPYW---NTDDVAAGYDIALRLAQSRTL 131
QY 258 RKFMKIGVSPPA 269
DB 132 NSYVQLGVLPRA 143

RESULT 15

ELRT1

pancreatic elastase (EC 3.4.21.36) I precursor - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 18-Aug-1982 #sequence_revision 18-Aug-1982 #text_change 09-Jul-2004
C;Accession: A00960; A20534
R;MacDonald, R.J.; Swift, G.H.; Quinto, C.; Swain, W.; Pictet, R.L.; Nikovits, W.; Rutte;
Biochemistry 21, 1453-1463, 1982
A;Title: Primary structure of two distinct rat pancreatic preproelastases determined by
A;Reference number: A00960; MUID:82182867; PMID:6918221
A;Accession: A00960
A;Molecule type: mRNA
A;Residues: 1-266 <MAC>
A;Cross-references: UNIPROT:P00773; GB:V01234; NID:g56088; PIDN:CAA24544.1; PID:g56089
R;Largman, C.
Biochemistry 22, 3763-3770, 1983
A;Title: Isolation and characterization of rat pancreatic elastase.

A;Reference number: A20534; MUID:84000385; PMID:6555050
A;Accession: A20534
A;Molecule type: protein
A;Residues: 17-37,'X',39-45 <LAR>
C;Superfamily: trypsin; trypsin homology
C;Keywords: hydrolase; pancreas; serine proteinase; zymogen
F;1-16/Domain: signal sequence #status predicted <SIG>
F;17-26/Domain: activation peptide #status predicted <APT>
F;27-266/Product: elastase I #status predicted <MPT>
F;27-259/Domain: trypsin homology <TRY>
F;71,119,214/Active site: His, Asp, Ser #status predicted

Query Match	5.4%	Score 113;	DB 1;	Length 266;
Best Local Similarity	26.7%	Pred. No. 0.076;		
Matches 39;	Conservative 23;	Mismatches 48;	Indels 36;	Gaps 7;
Qy	128	ROIYGYDSRFSIFGKDFLLNYPFSTSVKLSGTG-----CTGTLVAEKHVLTAACHIDGKT	182	
Db	26	RVVGGAEARRNSWPSQISLQY-----LSGGSWYHTCGGTLIIRNWMVMTAAHCVSQMT	78	
Qy	183	YVKGTOKLRVGFLLKPKFKDGGRGANDSTSAMPEQMKFQWIRVKETHVPKGIKGNANDIG	242	
Db	79	F-----RVVVG-----DHNLSQNDGTE-----QYVSVQKIMVHPTW---NSNNVA	115	
Qy	243	MDYDYALLEL-KKPKRKFVKIGVSP	267	
Db	116	AGYDIALRLAQSVTLNNYQLAVLP	141	

Search completed: July 1, 2005, 21:09:20
Job time : 21.3479 secs

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RP SEQUENCE FROM N.A.
 RC TISSUE=Cervix;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Shevchenko Y., Bouffard G.G.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 CC -1- SUBCELLULAR LOCATION: Secreted (Potential).
 CC -1- SIMILARITY: Belongs to the peptidase S1 family.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (see http://www.ebi.ac.uk/announcements/
 CC or send an email to license@sib-sib.ch).
 CC -----
 DR EMBL; AF015287; AAD01553.1; -
 DR EMBL; AF193611; AAR07186.1; -
 DR EMBL; ALJ36914; CAB66848.1; -
 DR EMBL; AY359033; AAR09392.1; -
 DR EMBL; BC001278; AAR01278.1; -
 DR MEROPS; S01.309; -
 DR H-InvDB; HIX0010006; -
 DR InterPro; IPR009003; Pept_Ser_Cys.
 DR InterPro; IPR001254; Peptidase_S1.
 DR InterPro; IPR001314; Peptidase_S1A.
 DR Pfam; PF00089; Trypsin; 1.
 DR PRINTS; PR00722; CHYMOTRYPSIN.
 DR SMART; SM00020; Tryp_SPC; 1.
 DR PROSITE; PS00240; TRYPSIN_DOM; FALSE_NEG.
 DR PROSITE; PS00134; TRYPSIN_HIS; 1.
 DR PROSITE; PS00135; TRYPSIN_SER; FALSE_NEG.
 DR KEGG; Hydrolase; Serine protease; Signal.
 FT SIGNAL 1 23 Potential.
 FT CHAIN 24 383 Serine protease 23.
 FT ACT_SITE 175 175 Charge relay system (By similarity).
 FT ACT_SITE 240 240 Charge relay system (By similarity).
 FT ACT_SITE 316 316 Charge relay system (By similarity).
 FT DISULFID 160 176 By similarity.
 FT CARBOHYD 93 93 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 207 207 N-linked (GlcNAc...) (Potential).
 FT SEQUENCE 383 AA; 43001 MW; 46EBE6C1ABFD5E9F CRC64;
 Query Match 100.0%; Score 2080; DB 1; Length 383;
 Best Local Similarity 100.0%; Pred. No. 6.2e-168;
 Matches 383; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MAGTGLGLFLFLFLLCAVGQSPYSAPWKTWPAYRLPVVLPQSTLNLAIXPDGAEAKLE 60
 DB 1 MAGTGLGLFLFLFLLCAVGQSPYSAPWKTWPAYRLPVVLPQSTLNLAIXPDGAEAKLE 60
 QY 61 VSSCGPQCHKGTPLPYEEAKQVLSYETLYANGSRRTQVGVIYLLSSGSGAQHRDSSG 120
 DB 61 VSSCGPQCHKGTPLPYEEAKQVLSYETLYANGSRRTQVGVIYLLSSGSGAQHRDSSG 120

QY 121 SGKSRKRQIYGYDSRFSIFGKDFLLNYPFSTSVKLTGCTGTGLVAEKHVLTAACHIDG 180
 DB 121 SGKSRKRQIYGYDSRFSIFGKDFLLNYPFSTSVKLTGCTGTGLVAEKHVLTAACHIDG 180
 QY 181 KTVVKGTKLRYGFLKPKFKDGGRGANDSTSAMPEQMKFQWIRVKETHVPKGIKGNAND 240
 DB 181 KTVVKGTKLRYGFLKPKFKDGGRGANDSTSAMPEQMKFQWIRVKETHVPKGIKGNAND 240
 QY 241 IGMVDYDYLLELKKPKRKFPMKIGVSPPAKQLPGGRIHFSGYDNDPRGNLVYRFCVDKDE 300
 DB 241 IGMVDYDYLLELKKPKRKFPMKIGVSPPAKQLPGGRIHFSGYDNDPRGNLVYRFCVDKDE 300
 QY 301 TYDLLYQQCDAOPGASGSGVYVMRWKQQQKWERKIIGIFSGHQWDMNGSPQDFNVAVR 360
 DB 301 TYDLLYQQCDAOPGASGSGVYVMRWKQQQKWERKIIGIFSGHQWDMNGSPQDFNVAVR 360
 QY 361 ITPLKYAQICYWKGNLYDCREG 383
 DB 361 ITPLKYAQICYWKGNLYDCREG 383
 RESULT 2
 Q6AY61 PRELIMINARY; PRT; 383 AA.
 ID Q6AY61 AC Q6AY61
 DT 25-OCT-2004 (TrEMBLrel. 28, Created)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
 DE Hypothetical protein
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 ON NCBI_TaxID=10116;
 RX [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Kidney;
 RC PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Shevchenko Y., Bouffard G.G.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
 Jones S.J., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Kidney;
 RC Director MGC Project;
 RL Submitted (AUG-2004) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: Belongs to peptidase family S1.
 DR EMBL; BC079179; AAR79179.1; -
 DR GO; GO:0000786; C:nucleosome; IEA.
 DR GO; GO:0005634; C:nucleus; IEA.
 DR GO; GO:0004263; F:chymotrypsin activity; IEA.
 DR GO; GO:0003677; F:DNA binding; IEA.
 DR GO; GO:0007001; P:chromosome organization and biogenesis (gen. . .); IEA.
 DR GO; GO:0006334; P:nucleosome assembly; IEA.
 DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
 DR InterPro; IPR001951; Histone_H4.
 DR InterPro; IPR001254; Peptidase_S1.

DR InterPro; IPR001314; Peptidase SIA.
 DR InterPro; IPR009003; Pept_Ser_Cys.
 DR Pfam; PF00089; Trypsin_1__Cys.
 DR PRINTS; PR00722; CHYMOTRYPSIN.
 DR ProDom; PD001827; Histone H4; 1.
 DR PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.
 KW Hydrolase; Hypothetical protein; Protease; Serine protease.
 SQ SEQUENCE 383 AA; 43159 MW; 4AB12CC7B66CDFC8 CRC64;

Query Match 91.5%; Score 1903; DB 2; Length 383;
 Best Local Similarity 91.4%; Pred. No. 6.4e-153;
 Matches 350; Conservative 11; Mismatches 22; Indels 0; Gaps 0;

QY 1 MAGIPGLFLLFLLCAVGQVSPYAPKPTWPAIRLPLVVLPOSTLNLAKPDCFAGAKLE 60
 DB 1 MAGIPGLLILLVLLCVFMQVSPNVPKPTWPAIRLPIVLPOSTLKLAKPDPFCAKLE 60

QY 61 VSSCGPQCHKGTPLPYEEAKQVLSYETLYANGSRTEQTQVGIYLSNGEGRAHSDGS 120
 DB 61 VSSCGPQCHKGTPLPYEEAKQVLSYETLYANGSRTEQTQVGIYLSNGEGRAHSDSEA 120

QY 121 SGKSRKQIYGVDSRISFGKDFLLNYPSTSVKLTGTGTTLVABKHVLTAAHCHIDG 180
 DB 121 AGKSRKQIYGVDSRISFGKDFLLNYPSTSVKLTGTGTTLVABKHVLTAAHCHIDG 180

QY 181 KTVYKGTQKLRVGLKPKFGDGGRGANDSTSAMPEQMKFQWIRKRVTHVPKGIKGNAND 240
 DB 181 KTVYKGTQKLRVGLKPKFGDGGRGANDSTSSALVEKMKFQWIRKRVTHVPKGIKGNAND 240

QY 241 IGMDDYVALLLEKPKHKKFMKIGVSPPAKQLPGRGHIFSGYDNDPFGNLYVRFCDVKDE 300
 DB 241 IGMDDYVALLLEKPKHKKFMKIGVSPPAKQLPGRGHIFSGYDNDPFGNLYVRFCDVKDE 300

QY 301 TYDLLYQQDAQPGASGSGVYVWMKQKQKWKRIIGFSGHWDVMDGSPQDFNVAVR 360
 DB 301 TYDLLYQQDAQPGASGSGVYVWMKQKQKWKRIIGFSGHWDVMDGSPQDFNVAVR 360

QY 361 ITPKVAQICWIKGNLYLDCREG 383
 DB 361 ITPKVAQICWIKGNLYLDCREG 383

RESULT 3

PS23_MOUSE STANDARD; PRT; 382 AA.

AC Q9D6X6; Q8V8G1;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 25-OCT-2004 (Rel. 45, Last annotation update)
 DE Serine protease 23 precursor (EC 3.4.21.-).
 GN Name=Prs823;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OC NCBI_TaxID=10090;
 RN [1]

SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Tongue;
 RX MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
 RA Okazaki Y., Furuno M., Kagakawa T., Adachi J., Bono H., Kondo S.,
 RA Nikaide I., Otsu N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
 RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,
 RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
 RA Schram L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
 RA Blake J.A., Brad D., Brusic V., Chothia C., Corbani L.E., Cousins S.,
 RA Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,
 RA Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
 RA Grimmond S., Guenich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
 RA Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,
 RA Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
 RA Maglott D.R., Maltais K., Marchionni L., McKenzie L., Miki H.,
 RA Nagashima T., Numata K., Okido T., Pavan W.J., Perteau G., Pesole G.,
 RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,

Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
 RA Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K.,
 RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
 RA Verardo R., Wagner L., Wahlstedt C., Wang Y., Watanabe Y., Wells C.,
 RA Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L.,
 RA Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
 RA Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
 RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
 RA Hara A., Hashizume M., Iotani K., Ishii Y., Itoh M., Kagawa I.,
 RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shingawa A.,
 RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
 RA Birney E., Hayashizaki Y.;
 RT "Analysis of the mouse transcriptome based on functional annotation of
 60,770 full-length cDNAs";
 RL Nature 420:563-573 (2002).
 RN [2]

SEQUENCE FROM N.A.
 RP TISSUE=Breast tumor;
 RC MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RX Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heif F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Uedin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullah S.J.,
 RA Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Vallalón D.K., Muny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S., Krzywinski M.I., Skalska U., Smailus D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 and mouse cDNA sequences";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 CC -1- SUBCELLULAR LOCATION: Secreted (Potential).
 CC -1- SIMILARITY: Belongs to the peptidase S1 family.

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 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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 CC or send an email to license@ebi.ac.uk).

 DR EMBL; AK009847; BAB26541.1; -;
 DR EMBL; AK078518; BAC37319.1; -;
 DR EMBL; BC018517; AAH18517.1; -;
 DR HSP; P00746; 1DSU.
 DR MEROPS; S01.309; -;
 DR MGD; MGI:1923703; 2310046G1Srik.
 DR InterPro; IPR009003; Pept_Ser_Cys.
 DR InterPro; IPR001254; Peptidase_S1.
 DR InterPro; IPR001314; Peptidase_S1A.
 DR Pfam; PF00089; Trypsin; 1.
 DR PRINTS; PR00722; CHYMOTRYPSIN.
 DR SMART; SM00020; Tryp_SPC; 1.
 DR PROSITE; PS0240; TRYPSIN_DOM; FALSE_NEG.
 DR PROSITE; PS00134; TRYPSIN_HIS; 1.
 DR PROSITE; PS00135; TRYPSIN_SER; FALSE_NEG.
 KW Hydrolase; Serine protease; Signal.
 FT SIGNAL 1 22 Potential.
 FT CHAIN 23 382 Serine protease 23.
 FT ACT_SITE 174 174 Charge relay system (By similarity).
 FT ACT_SITE 239 239 Charge relay system (By similarity).
 FT ACT_SITE 315 315 Charge relay system (By similarity).
 FT DISULFID 159 175 By similarity.
 FT CARBOHYD 92 92 N-linked (GlcNAc...) (Potential).

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FT CARBOHYD 206 206 N-linked (GlcNAc...) (Potential).
FT CONFLICT 260 260 M -> I (in Ref. 1; BAB26541).
SQ SEQUENCE 382 AA; 43071 MW; 6F09A5C80A5B2306 CRC64;

Query Match 90.8%; Score 1888.5; DB 1; Length 382;
Best Local Similarity 90.8%; Pred. No. 1.1e-151;
Matches 348; Conservative 14; Mismatches 20; Indels 1; Gaps 1;

QY 1 MAGIPGLLFLFLFLLCAVGVSPYSAPWKPTWPAYRLPVVLPQSTLNLAKEPFCBAKLE 60
DB 1 MAGIPG-LFILLVLLCVFMQVSPYTPWKPTWPAYRLPVVLPQSTLNLAKEPFCBAKLE 59

QY 61 VSSSCGQCHKGTPLPYIEAKQVLSYETLYANGSRTETQVGIYILSSSGDGAQHRS 120
DB 60 VSSSCGQCHKGTPLPYIEAKQVLSYETLYANGSRTETQVGIYILSSSGDGAQHRS 119

QY 121 SGKSRKRQIYGVDSRPSIFGKDFLLNYPSTSVKLSCTGCTGLVAEKHVLTAHC 180
DB 120 TGRSRRKRQIYGVDSRPSIFGKDFLLNYPSTSVKLSCTGCTGLVAEKHVLTAHC 179

QY 181 KTYVKGTKLRVGLFKPKFKDGGRGANDSTSAMPEQMKFQWIRVKTHTVPGWIKGN 240
DB 180 KTYVKGTKLRVGLFKPKFKDGGRGANDSTSAMPEQMKFQWIRVKTHTVPGWIKGN 239

QY 241 IGMDDYVALLLEKKPHRKPMKIGVSPAPKQLPGRIHFSGYNDRPGNLVYRFDVK 300
DB 240 IGMDDYVALLLEKKPHRKPMKIGVSPAPKQLPGRIHFSGYNDRPGNLVYRFDVK 299

QY 301 TYDLYOCCDAQPCASGSGVYVWMKQOQKWKRIIGIFSGHWDVMDGSPQDENVA 360
DB 300 TYDLYOCCDAQPCASGSGVYVWMKQOQKWKRIIGIFSGHWDVMDGSPQDENVA 359

QY 361 ITPLYAQICVWIKGNLYDCREG 383
DB 360 ITPLYAQICVWIKGNLYDCREG 382

RESULT 4
Q8BZS4 PRELIMINARY; PRT; 382 AA.
AC Q8BZS4
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DE Mus musculus adult male cecum cDNA, RIKEN full-length enriched
DE library, clone:913021B18 product:SRINE PROTEASE (HYPOTHETICAL 43.0
DE kDa PROTEIN) (PROTEASE, SERINE, 23) homolog.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Cecum;
RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA Carninci P., Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning.";
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Cecum;
RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA RIKEN FANTOM Consortium;
RT "Functional annotation of a full-length mouse cDNA collection.";
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Cecum;
RA The FANTOM Consortium;
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
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RN RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Cecum;
RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT "Normalization and subtraction of cap-crapper-selected cDNAs to
RT prepare full-length cDNA libraries for rapid discovery of new genes.";
RL Genome Res. 10:1617-1630(2000).
RN [5]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Cecum;
RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA Konno H., Akiyama J., Nishi K., Kitsuunai T., Tashiro H., Itoh M.,
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Hazada A.,
RA Yamanoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
RA Itoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system-384-format
RT sequencing pipeline with 384 multicapillary sequencer.";
RL Genome Res. 10:1757-1771(2000).
RN [6]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Cecum;
RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
RA Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
RA Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
RA Kurihara K., Matsuyama T., Miyazaki A., Murata M., Koda M., Koya S.,
RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
RA Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
RA Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
CC -I- SIMILARITY: Belongs to the EMBL/GenBank/DBJ databases.
DR EMBL; AK033671; BAC28420.1; -.
DR GO; GO:0004263; F:chymotrypsin activity; IEA.
DR GO; GO:0008233; F:peptidase activity; IEA.
DR GO; GO:0004295; F:trypsin activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR001254; Peptidase S1.
DR InterPro; IPR001314; Peptidase S1A.
DR InterPro; IPR009003; Pept Ser_Cys.
DR PRINTS; PR00722; CHYMOTRYPSIN_Cys.
DR SMART; SM00020; Tryp_Spc; 1.
DR PROSITE; PS00134; TRYPSIN_His; UNKNOWN 1.
DR Hydrolase; Hypothetical protein; Protease; Serine protease.
SQ SEQUENCE 382 AA; 43147 MW; 556789818E12A081 CRC64;

Query Match 90.5%; Score 1882.5; DB 2; Length 382;
Best Local Similarity 90.6%; Pred. No. 3.5e-151;
Matches 347; Conservative 14; Mismatches 21; Indels 1; Gaps 1;

QY 1 MAGIPGLLFLFLFLLCAVGVSPYSAPWKPTWPAYRLPVVLPQSTLNLAKEPFCBAKLE 60
DB 1 MAGIPG-LFILLVLLCVFMQVSPYTPWKPTWPAYRLPVVLPQSTLNLAKEPFCBAKLE 59

QY 61 VSSSCGQCHKGTPLPYIEAKQVLSYETLYANGSRTETQVGIYILSSSGDGAQHRS 120
DB 60 VSSSCGQCHKGTPLPYIEAKQVLSYETLYANGSRTETQVGIYILSSSGDGAQHRS 119

QY 121 SGKSRKRQIYGVDSRPSIFGKDFLLNYPSTSVKLSCTGCTGLVAEKHVLTAHC 180
DB 120 TGRSRRKRQIYGVDSRPSIFGKDFLLNYPSTSVKLSCTGCTGLVAEKHVLTAHC 179

QY 181 KTYVKGTKLRVGLFKPKFKDGGRGANDSTSAMPEQMKFQWIRVKTHTVPGWIKGN 240
DB 180 KTYVKGTKLRVGLFKPKFKDGGRGANDSTSAMPEQMKFQWIRVKTHTVPGWIKGN 239
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Qy	241	IGMDYDVALLELKPKHKEFKMGIVSPPAKQLPGGRIHPSGVDNDRPGNLVYRFGCDVDE	300		
Db	240	IGMDYDVALLELKPKHKEFKMGIVSPPAKQLPGGRIHPSGVDNDRPGNLVYRFGCDVDE	299		
Qy	301	TYDLLYQOCDAQPGASGSGVYVRMWKROQKWERKIIGIFSGHQWDMNGSPQDFNVAVR	360		
Db	300	TYDLLYQOCDAQPGASGSGVYVRMWKRPQKWERKIIGIFSGHQWDMNGSPQDFNVAVR	359		
Qy	361	ITPLKYAQICYWIKNGYLLDCREG 383			
Db	360	ITPLKYAQICYWIKNGYLLDCREG 382			
RESULT 5					
Q9BQP6	PRELIMINARY; PRT; 413 AA.				
AC	Q9BQP6				
DT	01-JUN-2001	(TRENBLrel. 17, Created)			
DT	01-JUN-2001	(TRENBLrel. 17, Last sequence update)			
DT	01-MAR-2004	(TRENBLrel. 26, Last annotation update)			
DE	DJ223E3.1	(Putative secreted protein ZS1313)			
GN	Name=DJ223E3.1;				
OS	Homo sapiens (Human).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
OX	NCBI_TaxID=9606;				
RN	[1]				
RP	SEQUENCE FROM N.A..				
RA	Dunn M.;				
RL	Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.				
CC	-1- SIMILARITY: Belongs to peptidase family S1.				
DR	EMBL; ALJ21939; CAC35071.1; -				
DR	MEROPS; S01.994; -				
DR	Genew; HGNC:21387; PRSS35.				
DR	GO; GO:0004263; F:chymotrypsin activity; IEA.				
DR	GO; GO:0008233; F:peptidase activity; IEA.				
DR	GO; GO:0004295; F:trypsin activity; IEA.				
DR	GO; GO:0006508; P:proteolysis and peptidolysis; IEA.				
DR	InterPro; IPR001254; Peptidase S1.				
DR	InterPro; IPR001314; Peptidase S1A.				
DR	InterPro; IPR003003; Pept_Ser_Cys.				
DR	Pfam; PF00089; Trypsin; 1.				
DR	PRINTS; PR00722; CHYMOTRYPSIN.				
DR	SMART; SM00020; Tryp_Spc; 1.				
DR	PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.				
KW	Hydrolase; Protease; Serine protease.				
SQ	SEQUENCE 413 AA; 47098 MW; 818D9C951BD2D6C1 CRC64;				
Query Match 50.1%; Score 1042; DB 2; Length 413;					
Best Local Similarity 47.8%; Pred. No. 7.7e-80;					
Matches 200; Conservative 68; Mismatches 100; Indels 50; Gaps 7					
Qy	7	LLLELLPELLCAVG--QVSPYSAPKPTWPAYRLPVLPQSLTLNLAQPPFGAEAKLEVSSS 64			
Db	5	LLMLIFP---TPGWTLDGSEMEWDFMHLRKVPRIVSERTFHLTSPAFADAKQMVNTV 61			
Qy	65	CGPOCHKGTPLPTVEEAKQYLSYETLYANGSKRTETOVGI--VILLSGSDGAQHRDSGSG 122			
Db	62	CGTECQELPTPSLEEDLYSYETVENGTRTLTRVKVQDLVLEPT-----QNTTKG 115			
Qy	123	KS-RRKQIYGYDSRSGIFGKDFLLNYPFSTSVKLSTGCTGTVAERHVLTAAHCIHDGK 181			
Db	116	VSVRRKQVYGTDSRSGIILDKRFLTNPPFPSTAVKLSGCSGLILSPQHVLTAACHVHDGK 175			
Qy	182	TYVKGTKLRVGLFKPKPKDGR-----GANDSTSMPEQMK----- 218			
Db	176	DYVKGSKLRVGLLKMKNKSGCKRGRSGKRREASGQDQREGTREHLRERAKGGRRRK 235			
Qy	219	-----FQWIRVRKTHVPKGIWKNANDIGMDYDVALLELKPKHKEFKMGIV 265			
Db	236	SGRQRTAEGRPSPQWTRVKVNTHTPKGWARGMGDATUDYDVALLELKRAHKCKTWEIGI 295			
Qy	266	SPPAKQLPGGRIHPSGVDNDRPGNLVYRFGCDVDEYDLLYQOCDAQPGASGSGVYVRMW 325			

Db 296 SPTIKQVGGHIFSGFDNRADQLVYRFCVSDESNDLLYQYCDABSGSTGSGVYLRUK 355
 Qy 326 KROQCKWERKIIGTIFSGHQWDMNGSPQDFNVAVRITPLKKAQICWYTKGNLYDCREG 383
 Db 356 DPDKCKWKRKLIAVYSGHQWVDHGVQKDYNVAVRITPLKKAQICLWTHGNDANCAYG 413

RESULT 6
 Q8N320 PRELIMINARY; PRT; 413 AA.
 ID Q8N320
 AC Q8N320;
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)
 DT 25-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
 DE Hypothetical protein PRSS35 (ENM522).
 GN Name=PRSS35; ORFNames=UNQ522;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RX MEDLINE=42386257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hong L.,
 RA Datchenko L., Marusina K., Farmer A.A., Rubin G.W., Hong F.,
 RA Scapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano B.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.C., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krzywinski M.I., Skalek U., Smalls D.E., Schnerch A., Schein J.E.,
 RA Jones S.J., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences."
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16999-16903(2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RA Strausberg R.;
 RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22887296; PubMed=12975309; DOI=10.1101/gr.1293003;
 RA Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D., Brush J.,
 RA Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,
 RA Eaton D., Foster J., Grimaldi C., Gu Q., Hass P.E., Heldens S.,
 RA Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,
 RA Lewis L., Liao D., Mark M., Robbie E., Sanchez C., Schoenfeld J.,
 RA Seehagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A.,
 RA Vandlen R., Watanabe C., Wiand D., Woods K., Xie M.H., Yanesura D.,
 RA Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I.,
 RA Godowski P.;
 RT "The secreted protein discovery initiative (SPDI), a large-scale
 RT effort to identify novel human secreted and transmembrane proteins: a
 RT bioinformatics assessment."
 RL Genome Res. 13:2265-2270(2003).
 CC -I- SIMILARITY: Belongs to peptidase family S1.
 DR EMBL: BC037170; AAH37170.1; -;
 DR EMBL: AY358661; AAC89024.1; -;
 DR GO: GO:0004263; F:chymotrypsin activity; IEA.
 DR GO: GO:0008233; F:peptidase activity; IEA.
 DR GO: GO:0004295; F:trypsin activity; IEA.
 DR GO: GO:0006508; P:proteolysis and peptidolysis; IEA.

RN [3] SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Testis;
RA The FANTOM Consortium;
RT "Analysis of the mouse transcriptome based on functional annotation of
RL 60,770 full-length cDNAs";
RN [4] Nature 420:563-573(2002).
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Testis;
RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RA Carninci P., Shibata Y., Hayatsu M., Sugahara Y., Shibata K., Itoh M.,
RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
RL prepare full-length cDNA libraries for rapid discovery of new genes";
RN [5] Genome Res. 10:1617-1630(2000).
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Testis;
RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA Shibata K., Itoh M., Aizawa K., Nagao S., Sasaki N., Carninci P.,
RA Konno H., Akiyama J., Nishi K., Kitsuana T., Tashiro H., Itoh M.,
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishino T., Harada A.,
RA Yamamoto R., Matsuoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA Fujiwaki S., Inoue K., Togawa Y., Izawa M., Ohara E., Watabiki M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
RA "Riken integrated sequence analysis (RISA) system-384-format
RL sequencing pipeline with 384 multicapillary sequencer";
RN [6] Genome Res. 10:1757-1771(2000).
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Testis;
RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
RA Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
RA Hori P., Imotani K., Ishii Y., Itoh M., Kigawa T., Kasukawa T.,
RA Kato H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,
RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
RA Saito H., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
RA Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
RA Tagawa A., Takahashi P., Takaku-Akaira S., Takeda Y., Tanaka T.,
RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK031644; BAC27491.1; -
DR MGD; MGI:2444800; Prs435.
DR GO; GO:0005615; C:extracellular space; TAS.
DR InterPro; IPR001254; Peptidease_S1.
DR Pfam; PF00089; Trypsin; 1.
DR SMART; SM00020; Tryp_Spc; 1.
DR KEGG; K00002; Serine protease.
SQ SEQUENCE 409 AA; 45736 MW; E9C9B91B6800719C CRC64;
Query Match 48.3%; Score 1005.5; DB 2; Length 409;
Best Local Similarity 48.8%; Pred. No. 9.5e-77;
Matches 191; Conservative 70; Mismatches 83; Indels 47; Gaps 5;
QY 31 TWPAYRLPVVLPSTLNLAKPDECAEAKLEVSSCGPQCHGTPLPTYEAKQYLSVETL 90
DB 28 TWHLRSIPQVSVNTHLASFPTQADAGVVKATVCGIECQEEPAPLSQLESLEYTI 87
QY 91 YANGSRTEQVGYIL-----SSSGDAQHRDSSGSGKRRRIQYIGYDSRFISFKDF 144
DB 88 FENGTRTLTRVKQGLVLETRNVSVKGAH-----PRRRQVGTDSRFSILDKRF 138
QY 145 LLNYPSTSVKLSGCTGCTTVAEKHVLTAACHIDGKTYVKGTKRVLGFKPKFDG-- 202
DB 139 ATNFPFNTAVKLSGCTGLVSPNHLTAANCVDHGDYKVGSKLRLVGLKRNKGRK 198
QY 203 -GRGA-----NDSTSMPQEQ-----KQWIRVVRTHVPKG 232

DB 199 KREGKRSRREAESAGSOAHLRESITQRPCKSRGRPRVTQCRPSFQWTRVASTHPKG 258
QY 233 WIKGNANDIGMDYDVALLELKKPKKFKMKIGVSPPAKQLPGRIHFSGVDNDRPGLVY 292
DB 259 WVRGNGGLDLYDVALLELKKRAHQHMLGVSPTITLPGQIHFGFNDNRDEQLVY 318
QY 293 RFGCDVDETVLLYQCDAPGASGSGVYVVMKROQKWKRTIGTFSGHGVMDNNGSP 352
DB 319 RFGSVSEESNDLLYQYCDAGSTSGGIYLRLEKPGQKWKRIKIVAVYSGHQWVDVHGQV 378
QY 353 QDFNVAVRITPLKYAQICYMIKGNLYDCREG 383
DB 379 KQNVAVRITPLKYAQICLWIHGNAANCAVG 409
RESULT 11
GSEP_BACLI STANDARD; PRT; 316 AA.
AC P80057;
DT 01-MAY-1992 (Rel. 22, Created)
DT 01-OCT-1993 (Rel. 27, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Glutamy1 endopeptidase precursor (EC 3.4.21.19) (Glutamate specific
GN endopeptidase) (GSE).
GN Name=blase;
OS Bacillus licheniformis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1402;
[1]
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RC STRAIN=ATCC 14580;
RX MEDLINE=93054737; PubMed=1429718;
RA Kakudo S., Kikuchi N., Kitadokoro K., Fujiwara T., Nakamura E.,
RA Okamoto H., Shin M., Tamaki M., Teraoka H., Tezuka H., Yoshida N.;
RT "Purification, characterization, cloning, and expression of a glutamic
RT acid-specific protease from Bacillus licheniformis ATCC 14580";
RN J. Biol. Chem. 267:23782-23788(1992).
RL [2]
SEQUENCE OF 95-316.
RP MEDLINE=92155199; PubMed=1346764;
RX Svendsen I., Breddam K.;
RT "Isolation and amino acid sequence of a glutamic acid specific
RT endopeptidase from Bacillus licheniformis";
RL Eur. J. Biochem. 204:165-171(1992).
CC -!- FUNCTION: Specific for hydrolysis of peptide bonds on the carboxyl
CC side of acidic amino acid residues, with a strong preference for
CC Glu.
CC -!- CATALYTIC ACTIVITY: Preferential cleavage: Asp|-Xaa, Glu|-Xaa.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the peptidase S1B family.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC
CC EMBL; D10060; BAA00949.1; -
DR PIR; A45134; A45134.
DR MEROPS; S01.271; -
DR InterPro; IPR000126; Pept_S1B_AS.
DR InterPro; IPR009003; Pept_Ser_Cys.
DR InterPro; IPR001254; Peptidase_S1.
DR InterPro; IPR008256; Peptidase_S1B.
DR Pfam; PF00089; Trypsin; 1.
DR PRINTS; PR00839; V8PROTEASE.
DR SMART; SM00020; Tryp_Spc; 1.
DR PROSITE; PS00672; V8_HIS; 1.
DR PROSITE; PS00673; V8_SER; 1.
KW Direct protein sequencing; Hydrolase; Serine protease; Signal.

```
FT SIGNAL 1 30 Potential.
FT PROPEP 31 94
FT CHAIN 95 316 Glutamyl endopeptidase.
FT ACT_SITE 141 141 Charge relay system (By similarity).
FT ACT_SITE 261 261 Charge relay system (By similarity).
FT DISULFID 126 142
FT DISULFID 275 279
SQ SEQUENCE 316 AA; 33611 MW; 96D7552CB7089B09 CRC64;

Query Match 9.3%; Score 194; DB 1; Length 316;
Best Local Similarity 24.0%; Pred. No. 4.8e-08;
Matches 79; Conservative 43; Mismatches 143; Indels 64; Gaps 15;

QY 63 SSCGPOCHKGTPL---PTYEEAKQYLSYETLYANGSRRTETQVGIYILSSSGDGAQHRDGS 119
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 28 AQAAPSPH--TPVSSDPSY-KAETSVTYDP-----NIKSDQYGLYSKAFGTGKVNETKE 79
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 120 SSGKSRKRQIYGVDSRFSIFGKDFLLN-----YPFSTSVKLST---CCTGLTVAEKHV 170
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 80 KAEKKSAPAKPY---SIKSVIGSDDRTRVTNTTAYPYRAIVHSSIGSCTGMIGPKTV 136
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 171 LTAACHICHDGKT-YVKGTOQLRVGFLKPKFKDGGRGANDSTSAMPEQMKFQWIRVXKTHV 229
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 137 ATAGHCIDYDTSSGSFAGTATVSPG-----RNGTS-----YPYGSVKSTRYFI 178
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 230 PKGWIKGNANDIGMDYDYLALKEKPKHKFKMKGIVSPPAKQLPGGRIHFSGYDNDRPGN 289
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 179 PSGRWSGNTN-----YDGAIELSEPIGNTVGVFGYSYTTSSLVGTTVTITISGYPGDKTAG 233
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 290 LVYRFCD--VKDETVDLLYQCDQAQPGASGSGYVYVMWKRQOQKWERKII----GIFSGH 343
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 234 TQWQHSPIAISETYKLOYAM-DTYGGSGSPVFQSSSRSTNCSGPCSLAVHTNGVYGG- 291
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 344 QWVDMNGSPQDFNVAVRITPLKYAICYW 372
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 292 -----SSYNRGTRITKEVFDNLTNW 311
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 12
ID Q65NR6 PRELIMINARY; PRT; 316 AA.
AC Q65NR6;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DE Mpr (EC 3.4.21.19) (Glutamyl Endo peptidase).
GN Name: mpr; ORFName: BL01804, BLI00340;
OS Bacillus licheniformis DSM 13.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=279010;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=DSM 13;
RX PubMed=15383718;
RA Veith B., Herzberg C., Steckel S., Feesche J., Maurer K.H.,
RA Ehrenreich P., Baumer S., Henne A., Liesegang H., Merkl R.,
RA Ehrenreich A., Gottschalk G.;
RT "The Complete Genome Sequence of Bacillus licheniformis DSM13, an
RT Organism with Great Industrial Potential.";
RL J. Mol. Microbiol. Biotechnol. 7:204-211(2004).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 14580;
RA Rey M.W., Ramaiya P., Nelson B.A., Brody-Karpin S.D., Zaretsky E.J.,
RA Tang M., de Leon A.L., Xiang H., Gueti V., Clausen I.G., Olsen P.B.,
RA Rasmussen M.D., Andersen J.T., Jorgensen P.L., Larsen T.S.,
RA Sorokin A., Bolotin A., Lapidus A., Galleron N., Ehrlich S.D.,
RA Berka R.M.;
RT "Complete genome sequence of the industrial bacterium Bacillus
RT licheniformis and comparisons with closely related Bacillus species.";
RL Genome Biol. 5:R77-R77(2004).
DR EMBL; AE017333; AAU39298.1; -.
DR EMBL; CP000002; AAU21945.1; -.

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KW Hydrolase.
SQ SEQUENCE 316 AA; 33611 MW; 96D7552CB7089B09 CRC64;

Query Match 9.3%; Score 194; DB 2; Length 316;
Best Local Similarity 24.0%; Pred. No. 4.8e-08;
Matches 79; Conservative 43; Mismatches 143; Indels 64; Gaps 15;

QY 63 SSCGPOCHKGTPL---PTYEEAKQYLSYETLYANGSRRTETQVGIYILSSSGDGAQHRDGS 119
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 28 AQAAPSPH--TPVSSDPSY-KAETSVTYDP-----NIKSDQYGLYSKAFGTGKVNETKE 79
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 120 SSGKSRKRQIYGVDSRFSIFGKDFLLN-----YPFSTSVKLST---CCTGLTVAEKHV 170
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 80 KAEKKSAPAKPY---SIKSVIGSDDRTRVTNTTAYPYRAIVHSSIGSCTGMIGPKTV 136
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 171 LTAACHICHDGKT-YVKGTOQLRVGFLKPKFKDGGRGANDSTSAMPEQMKFQWIRVXKTHV 229
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 137 ATAGHCIDYDTSSGSFAGTATVSPG-----RNGTS-----YPYGSVKSTRYFI 178
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 230 PKGWIKGNANDIGMDYDYLALKEKPKHKFKMKGIVSPPAKQLPGGRIHFSGYDNDRPGN 289
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 179 PSGRWSGNTN-----YDGAIELSEPIGNTVGVFGYSYTTSSLVGTTVTITISGYPGDKTAG 233
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 290 LVYRFCD--VKDETVDLLYQCDQAQPGASGSGYVYVMWKRQOQKWERKII----GIFSGH 343
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 234 TQWQHSPIAISETYKLOYAM-DTYGGSGSPVFQSSSRSTNCSGPCSLAVHTNGVYGG- 291
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 344 QWVDMNGSPQDFNVAVRITPLKYAICYW 372
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 292 -----SSYNRGTRITKEVFDNLTNW 311
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 13
QY1YES
ID Q71YES PRELIMINARY; PRT; 450 AA.
AC Q71YES;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Serine protease, putative.
GN OrderedLocusNames=LMOF2365.1900;
OS Listeria monocytogenes (serotype 4b / strain F2365).
OC Bacteria; Firmicutes; Bacillales; Listeriaceae; Listeria.
OX NCBI_TaxID=265669;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=15115801; DOI=10.1093/nar/gkh562;
RA Nelson K.E., Fouts D.E., Mongodin E.F., Ravel J., DeBoy R.T.,
RA Kolonay J.F., Rasko D.A., Angiuoli S.V., Gill S.R., Paulsen I.T.,
RA Peterson J.D., White O., Nelson W.C., Nierman W.C., Beanan M.J.,
RA Brinkac L.M., Daugherty S.C., Dodson R.J., Durkin A.S., Madupu R.,
Raft D.H., Selengut J., Van Aken S.E., Kouri H.M., Fedorova N.,
RA Forberger H.A., Tran B., Kathariou S., Wondolring L.D., Uhlich G.A.,
RA Bayles D.O., Luchansky J.B., Fraser C.M.;
RA "Whole genome comparisons of serotype 4b and 1/2a strains of the food-
RT borne pathogen Listeria monocytogenes reveal new insights into the
RT core genome components of this species.";
RL Nucleic Acids Res. 32:2386-2395(2004).
DR EMBL; AE017328; BA004669.1; -.
DR GO; GO:0004295; P:trypsin activity; IEA.
DR GO; GO:0008508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR006637; Chw.
DR InterPro; IPR001254; Peptidase_S1.
DR InterPro; IPR008256; Peptidase_S1B.
DR InterPro; IPR009003; Pept_Ser_Cys.
DR Pfam; PF07538; Chw; 3.
DR PRINTS; PR00839; V8PROTEASE.
DR SMART; SM00728; Chw; 3.
DR PROSITE; PS00240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN 1.
KW Complete proteome; Hydrolase; Protease; Serine protease.
SQ SEQUENCE 450 AA; 48793 MW; 54C79A67510PAD4A CRC64;

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	Query Match	9.0%; Score 188; DB 2; Length 450;
	Best Local Similarity	25.9%; Pred.No.2.4e-07;
	Matches	70; Conservative 43; Mismatches 85; Indels 72; Gaps 13;
Qy	128	RQIYGYDSRSIFGKDFLLN---YPFSTS-----VKLSTGCT----GTIVAETHVLTAAHC 176 :: : ::
Db	93	KTIFFGGD-----GRKLVTNTTPYSTSAYLVMEFPNGKTYIGSGQLIGEDSVLTAAHC 146 :: :: ::
Qy	177	IHDGKTVYVGTKLRVGFLEPKFKDDG-----RGANDSTSAMPQMKFWIVRVKRTH 228 :: -----
Db	147	LY-GK-----KDGWAKKVTVPGYNGT-----KAPFGTAKARMY 181 :: -----
Qy	229	VPGKWIKGNANDIGMDYDYALLELKPHKKRKMKIGVSPPAQLPQGRIHFHSGVDNDPRG 288 :: :: ::
Db	182	VPKEWTKKPS----TEDYGWLKDKNIGTKGTWGLTTNT----SCAIIISGVHGDKKG 233 :: :: ::
Qy	289	NLYVRFCVDKETVDLLYQQCDAPQAGSGVGSVVYVMWKROOQKWERKIIGIFSOGWVDM 348 :: :: :: ::
Db	234	KLVTQTGNISQVTAANNFYRLDTTGGSSGSGVY-----NSKKQILAV-NAYEYLNG 283 :: :: :: ::
Qy	349	NGSPQDFNVAVRTPLKYAQICYWIKNYL 378
Db	284	TGD-----NFGTRITKEKLNNIYTWAFFNNL 309

```

RESULT 14
Q98GI7
ID Q98GI7 PRELIMINARY; PRT; 364 AA.
AC Q98GI7;
DT 01-OCT-2001 (TrEMBLrel. 18, Created)
DT 01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Glutamyl endopeptidase (EC 3.4.21.19).
GN OrderedLocusNames=ml13306;
GS Rhizobium loti (Mesorhizobium loti).
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Phyllobacteriaceae; Mesorhizobium.
OX NCBI_TaxID=381;
[1]
SEQUENCE FROM N. A.
RP STRAIN=MAFF303099;
RC MEDLINE=21082930; PubMed=11214968;
RA Kaneko T., Nakamura Y., Sato S., Asamizu E., Kato T., Sasamoto S.,
RA Watanabe A., Iidesawa K., Ishikawa A., Kawashima K., Kimura T.,
RA Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsuno A.,
RA Takeuchi Y., Nakayama S., Nakazaki N., Shimpo S., Sugimoto M.,
RA Mochizuki C., Yamada M., Tabata S.;
RT "Complete genome structure of the nitrogen-fixing symbiotic bacterium
RT Mesorhizobium loti.";
RL DNA Res. 7:331-338(2000).
DR EMBL; AP003001; BAB50229.1; -.
DR GO; GO:0004295; F:trypsin activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR001254; Peptidase_S1.
DR InterPro; IPR008256; Peptidase_S1B.
DR Pfam; PF00089; Trypsin_1.
DR PRINTS; PR00839; V8PROTEASE.
DR SMART; SM00020; TRYD_SPC; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.
KW Complete proteome, Hydrolase, Protease; Serine protease.
SQ SEQUENCE 364 AA; 39034 MW; 13BE653270E7CDD3 CRC64;

```

```

Query Match      8.6%; Score 178.5; DB 2; Length 364;
Best Local Similarity 27.1%; Pred. No. 1.2e-06;
Matches 78; Conservative 43; Mismatches 114; Indels 53; Gaps 16;

QY    107 SSSGDAQHR-DSSGSKSRKRQIVGYDVRRESIFGDLLNYPFS-----SVKLST 158
       :.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.
Db     112 ANGADGRTERDPGLGEAGAQVFPDRREQVRNTK---TTPFSAIGYLEAKSANTGS 168
       :.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.

QY    159 --GCTGTVAERHVLTAAHCI--HDGTYTVYKGTKLRVGFLPKFKPDGGRGANDSTAMP 214
       :.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.

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Db      169 YGSCSATLIGRTVLTAAHCLYSHEDKDWL---SEYLFV-----PGLNGSTA--- 215
Qy      215 EQMKFQIRVYKVRTHVPKGWIKGNANDIG---MDYDYALLELKKPKRKFMKIGVSPPAQOL 272
Db      213 DDAPFGAFTVESAVLQGFIDNYQGYGVSPWDLGIIITLKLQDVGCTNLGWLGYA-NYDDL 271
Qy      273 PGGRIHFSQYNDNRP-GNLVYRFDVVKDETVDLLYQO---CDAQFCASGSGVYVRMWKQO 329
Db      272 GDFTFANLVGPGDKPMGTMWKASCVEVHAENITAFYFQDCTDTPFGSSGSSVYAYDTKSKQ 331
Qy      330 QKWERKIIGFISGHQWDMNGSPDFFNVAVRITLTKVAQICYWTIKGNY 377
Db      332 R-----IITG---VNVAESP-DANTAVRLN-----AANVQWINSLY 363

RESULT 15
Q987W6
ID Q987W6 PRELIMINARY; PRT; 271 AA.
AC Q987W6;
DT 01-OCT-2001 (TrEMBLrel. 18, Created)
DT 01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Glutamic acid specific endopeptidase.
GN OrderedLocusNames=ml16878;
OS Rhizobium loti (Mesorhizobium loti).
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Phyllobacteriaceae; Mesorhizobium.
OX NCBI_TaxID=381;
RN [1]
RS SEQUENCE FROM N.A.
RC STRAIN=MAFF303099;
RX MEDLINE=21082930; PubMed=11214968;
RA Kaneko T., Nakamura Y., Sato S., Asamizu E., Kato T., Sasamoto S.,
RA Watanabe A., Igesawa K., Ishikawa A., Kawashima K., Kimura T.,
RA Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsuno A.,
RA Mochizuki Y., Nakayama S., Nakazaki N., Shimpo S., Sugimoto M.,
RA Takeuchi C., Yanada M., Tabata S.;
RT "Complete genome structure of the nitrogen-fixing symbiotic bacterium
RT Mesorhizobium loti.";
RL DNA Res. 7:331-338(2000).
RC -1- SIMILARITY: Belongs to peptidase family S1.
DR EMBL; AP003010; BAB53084.1; -.
DR GO; GO:0004263; F:chymotrypsin activity; IEA.
DR GO; GO:0004295; F:trypsin activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR001254; Peptidase_S1.
DR InterPro; IPR001314; Peptidase_S1B.
DR InterPro; IPR009003; Pept_Ser_Cys.
DR Pfam; PF00089; Trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR PRINTS; PR00839; V8PROTEASE.
DR SMART; SM00020; Tryp_SPC; 1.
DR PROSITE; PS00240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN 1.
KW Complete proteome; Hydrolase; Protease; Serine protease.
SQ SEQUENCE 271 AA; 30385 MW; 37659307C63D0D9C CRC64;

```

	Query Match	7.6%	Score 158;	DB 2;	Length 271;
	Best Local Similarity	29.0%;	Pred. No. 4.5e-05;		
	Matches	67;	Mismatches	90;	Indels
					Gaps
					121
Qy	158	TGCTGTILVAEKHVLTAACHTIDHGKTYVYKGQTQLRVGF-LKPFPKDGGRGANDSTSAMEPQ	216	:	
		: :	: :		
Db	56	TGCTAFLLISPTRLTLAAHCITSPIQRLGLPNLVARIVTP-----GRASRD-----ARP----	105		
Qy	217	MKFQWIRVRKTHV-----PKGWIKGNANDIGMDYDYALLEKKPHKRKFMKICVSPPA	269	:	
		:	: :		
Db	106	--EGWKQAKWHVNPPYRRRPSGL-----HDVGLELERPFSPSPGHFQLWSNP	152		
Qy	270	KQ-----LPCCR-IHFSGYNDRNGNLVYRFCDVKDE--TYDLLLLYOOCDAQPGASGSVVYR	323	:	
		:	: :		
Db	153	RODLERLNTRLHHISGYPADKPDGTOWEHSERLDITEROLFYSVDTCPGHSAIPV----	209		

Qy 324 MWKRQOQKWERKIIGI-----FSGHQWVDMNGSPQD-----ENVAVRITP 363
Db 210 -WIHRQOAGPPVVIHVHTAGPRPHSGGANGCRPGVPLAPAGLENRGVRLTP 259

Search completed: July 1, 2005, 21:08:13
Job time : 91.581 secs